

Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	
			100					105					110			
aac	acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggc	gca	ggc	384
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	
		115					120					125				
tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggg	cgc	gag	tgg	gat	gaa	ctt	ctg	432
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	
	130					135					140					
gag	aag	gac	cag	gat	ggg	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser	
145					150				155						160	
gat	ggg	gac	tac	cag	acc	ttc	aag	gct	aac	gac	ggc	gca	tat	gtt	cgt	528
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	
				165				170						175		
gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn	
			180					185					190			
atg	acc	gac	gaa	gaa	atc	tgg	aag	ctt	cca	cgt	ggc	ggc	cac	gat	tac	624
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	
		195					200					205				
cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	
	210					215					220					
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	
225					230					235					240	
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	
				245					250					255		
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	
		260						265					270			
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggg	864
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	
		275					280					285				
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu	
	290					295					300					
ggg	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val	
305					310					315					320	
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	
				325					330					335		
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	

340	345	350	
cgc gat aag ggc ttg gct gat	cgc ctt gtc cca atc att cct gat gag	1104	
Arg Asp Lys Gly Leu Ala Asp	Arg Leu Val Pro Ile Ile Pro Asp Glu		
355	360	365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152		
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr			
370	375	380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200		
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu			
385	390	395	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248		
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn			
405	410	415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc tcc tac gcc	1296		
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala			
420	425	430	
acc cac ggc aag gcc atg att ccg ctg tac atc ttc tac tcg atg ttc	1344		
Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe			
435	440	445	
ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg	1385		
Gly Ile Pro Ala His Arg			
450			

<210> 102

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
1 5 10 15

Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
20 25 30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
35 40 45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
65 70 75 80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
85 90 95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
100 105 110

Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
115 120 125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
 420 425 430
 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
 435 440 445
 Gly Ile Pro Ala His Arg

450

<210> 103
 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1287)
 <223> FRXA02897

<400> 103
 gat ctc gat ggc ttc cgt cag gaa gtt tcc cgt gag cag ggt ggc att 48
 Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
 1 5 10 15

ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30

act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60

cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125

tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160

gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt 528
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175

gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
195 200 205	
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
210 215 220	
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
225 230 235 240	
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
275 280 285	
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
290 295 300	
ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
340 345 350	
cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
355 360 365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
370 375 380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
385 390 395 400	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
405 410 415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc	1287
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr	
420 425	

<210> 104

<211> 429

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
 1 5 10 15

Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110

Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140

Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160

Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175

Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190

Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205

Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220

Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240

Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270

Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285

Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
 420 425

<210> 105
 <211> 1133
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(1110)
 <223> RXN03083

<400> 105
 attcagcagt aatcatttag acttggaacc gcttaccagt gggtttcaaca atgcattcac 60
 ccagctcaca cgtgtggagg tgccttaatg gca aag agg atc gta att atc ggc 114
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac	354
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp	
75 80 85	
ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca	402
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser	
90 95 100 105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc	450
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr	
110 115 120	
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	498
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu	
125 130 135	
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	546
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro	
140 145 150	
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	594
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp	
155 160 165	
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val	
170 175 180 185	
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu	
190 195 200	
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His	
205 210 215	
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	786
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg	
220 225 230	
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr	
235 240 245	
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr	
250 255 260 265	
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp	
270 275 280	
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc	978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile	
285 290 295	
aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag	1026
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln	
300 305 310	
gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg	1074

Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325
 gcc gta tcg cca tgt atc acg cac tcg gtg aag gcg tgagcccat 1120
 Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
 330 335 340
 ccgtttgaag act 1133
 <210> 106
 <211> 341
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 106
 Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
 1 5 10 15
 Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
 20 25 30
 Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45
 Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60
 Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80
 Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95
 Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110
 Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125
 Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140
 Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160
 Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175
 Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190
 Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205
 Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220
 Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240

Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
 275 280 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
 290 295 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
 305 310 315 320

His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
 325 330 335

His Ser Val Lys Ala
 340

<210> 107
 <211> 1518
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (89)..(1495)
 <223> FRXA02853

<400> 107
 aattcagcag taatcattta gacttggaac cgcttaccag tggtttcaac aatgcattca 60

cccagctcac acgtgtggag gtgccttaatg gca aag agg atc gta att atc ggc 115
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25

gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
 75 80 85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser

90	95	100	105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc				451
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr	110	115	120	
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa				499
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu	125	130	135	
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc				547
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro	140	145	150	
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg				595
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp	155	160	165	
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt				643
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val	170	175	180	185
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc				691
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu	190	195	200	
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac				739
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His	205	210	215	
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc				787
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg	220	225	230	
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc				835
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr	235	240	245	
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac				883
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr	250	255	260	265
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat				931
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp	270	275	280	
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc				979
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile	285	290	295	
aag gtt gac cgn gtc tcc cgc acc aac atc ccc ggt gtg tac gca gca				1027
Lys Val Asp Arg Val Ser Arg Thr Asn Ile Pro Gly Val Tyr Ala Ala	300	305	310	
ggt gac tgt act gac cta ttc cca ctg gcg tcc gtt gca gcg atg cag				1075
Gly Asp Cys Thr Asp Leu Phe Pro Leu Ala Ser Val Ala Ala Met Gln	315	320	325	
ggc cgt atc gcc atg tat cac gca ctc ggt gaa ggc gtg agc ccc atc				1123
Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile	330	335	340	345

cgt ttg aag act gtt gcc acc gca gtg ttt acc cgc cca gag atc gca 1171
 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala
 350 355 360

gca gta ggt atc acc cat gca caa gtt gat tcc ggc gaa gtg tct gct 1219
 Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala
 365 370 375

cgc gtg att gtg ctt cct ttg gct act aac cca cgc gcc aag atg cgt 1267
 Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg
 380 385 390

tcc ctg cgc cac ggt ttt gtg aag ctg ttc tgc cgc cgt aac tct ggc 1315
 Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly
 395 400 405

ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc 1363
 Leu Ile Ile Gly Gly Val Val Val Ala Pro Thr Ala Ser Glu Leu Ile
 410 415 420 425

cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg 1411
 Leu Pro Ile Ala Val Ala Val Thr Asn Arg Leu Thr Val Ala Asp Leu
 430 435 440

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu
 445 450 455

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505
 Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly
 460 465

gagtcttaga ttt 1518

<210> 108

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
1 5 10 15

Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
20 25 30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly

100					105					110				
Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile	115				120					125				
Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu	130				135					140				
Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu	145				150					155			160	
Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu				165				170					175	
Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala				180				185					190	
Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val				195				200					205	
Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp				210				215					220	
Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His				225				230					235	
Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val				245				250					255	
Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr				260				265					270	
Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly				275				280					285	
Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Val Ser Arg				290				295					300	
Thr Asn Ile Pro Gly Val Tyr Ala Ala Gly Asp Cys Thr Asp Leu Phe				305				310					315	
Pro Leu Ala Ser Val Ala Ala Met Gln Gly Arg Ile Ala Met Tyr His				325				330					335	
Ala Leu Gly Glu Gly Val Ser Pro Ile Arg Leu Lys Thr Val Ala Thr				340				345					350	
Ala Val Phe Thr Arg Pro Glu Ile Ala Ala Val Gly Ile Thr His Ala				355				360					365	
Gln Val Asp Ser Gly Glu Val Ser Ala Arg Val Ile Val Leu Pro Leu				370				375					380	
Ala Thr Asn Pro Arg Ala Lys Met Arg Ser Leu Arg His Gly Phe Val				385				390					395	
Lys Leu Phe Cys Arg Arg Asn Ser Gly Leu Ile Ile Gly Gly Val Val				405				410					415	
Val Ala Pro Thr Ala Ser Glu Leu Ile Leu Pro Ile Ala Val Ala Val				420				425					430	

Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
 435 440 445

Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln
 450 455 460

His Asp Asp Leu Gly
 465

<210> 109

<211> 2895

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2872)

<223> RXA02259

<400> 109

atgagcccat gaaagccatc gaaatcaatc gccagctaa acacctgttt tgctgggtga 60

ttttttatct catgcacgcc aacaccctca atgtgaaaga gtg ttt aaa gta gtt 115
 Val Phe Lys Val Val
 1 5

atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc 163
 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
 10 15 20

ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211
 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
 25 30 35

gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa 259
 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
 40 45 50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307
 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
 55 60 65

aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355
 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
 70 75 80 85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403
 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
 90 95 100

ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451
 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
 105 110 115

aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat 499
 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
 120 125 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc 547

Ala	Glu	Val	Ala	Pro	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Thr	Arg	Arg		
135						140					145						
cgc	act	gtt	ttt	gat	gcg	caa	aag	tgg	atc	acc	acc	cac	atg	cgt	gaa	595	
Arg	Thr	Val	Phe	Asp	Ala	Gln	Lys	Trp	Ile	Thr	Thr	His	Met	Arg	Glu		
150					155					160					165		
cgc	cac	gct	ttg	cag	tct	gcg	gag	cct	acc	gct	cgt	acg	caa	agc	aag	643	
Arg	His	Ala	Leu	Gln	Ser	Ala	Glu	Pro	Thr	Ala	Arg	Thr	Gln	Ser	Lys		
				170					175					180			
ttg	gat	gag	atc	gag	aag	aac	atc	cgc	cgt	cgc	atc	acc	att	ttg	tgg	691	
Leu	Asp	Glu	Ile	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Ile	Thr	Ile	Leu	Trp		
			185					190					195				
cag	acc	gcg	ttg	att	cgt	gtg	gcc	cgc	cca	cgt	atc	gag	gac	gag	atc	739	
Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
		200					205					210					
gaa	gta	ggg	ctg	cgc	tac	tac	aag	ctg	agc	ctt	ttg	gaa	gag	att	cca	787	
Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Ile	Pro		
		215				220					225						
cgt	atc	aac	cgt	gat	gtg	gct	gtt	gag	ctt	cgt	gag	cgt	ttc	ggc	gag	835	
Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	Arg	Glu	Arg	Phe	Gly	Glu		
230					235					240					245		
ggt	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggt	tcc	tgg	att	ggt	gga	883	
Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly	Ser	Trp	Ile	Gly	Gly		
				250					255					260			
gac	cac	gac	ggt	aac	cct	tat	gtc	acc	gcg	gaa	aca	gtt	gag	tat	tcc	931	
Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	Glu	Thr	Val	Glu	Tyr	Ser		
			265					270					275				
act	cac	cgc	gct	gcg	gaa	acc	gtg	ctc	aag	tac	tat	gca	cgc	cag	ctg	979	
Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
			280				285					290					
cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cgc	atg	aat	aag	gtc	1027	
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
		295				300					305						
acc	ccg	cag	ctg	ctt	gcg	ctg	gca	gat	gca	ggg	cac	aac	gac	gtg	cca	1075	
Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro		
310					315					320					325		
agc	cgc	gtg	gat	gag	cct	tat	cga	cgc	gcc	gtc	cat	ggc	gtt	cgc	gga	1123	
Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
				330					335				340				
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171	
Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu		
			345					350					355				
ggc	gtg	tgg	ttc	aag	gtc	ttt	act	cca	tac	gca	tct	ccg	gaa	gaa	ttc	1219	
Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		
		360					365					370					
tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267	
Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	Arg	Glu	Ser	Lys	Asp		

375	380	385	
gtt ctc att gcc gat gat cgt ttg tct gtg ctg att tct gcc atc gag Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu Ile Ser Ala Ile Glu 390 395 400 405			1315
agc ttt gga ttc aac ctt tac gca ctg gat ctg cgc caa aac tcc gaa Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu 410 415 420			1363
agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr 425 430 435			1411
gca aac tac cgc gag ctg tct gaa gca gag aag ctt gag gtg ctg ctg Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu 440 445 450			1459
aag gaa ctg cgc agc cct cgt ccg ctg atc ccg cac ggt tca gat gaa Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu 455 460 465			1507
tac agc gag gtc acc gac cgc gag ctc ggc atc ttc cgc acc gcg tcg Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser 470 475 480 485			1555
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile 490 495 500			1603
tcc atg gca tca tcg gtc acc gat gtg ctc gag ccg atg gtg ttg ctc Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu 505 510 515			1651
aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr 520 525 530			1699
gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly 535 540 545			1747
gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr 550 555 560 565			1795
ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp 570 575 580			1843
tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp 585 590 595			1891
gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu 600 605 610			1939
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro 615 620 625			1987

tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser 630 635 640 645	2035
gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn 650 655 660	2083
ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu 665 670 675	2131
gag gca tcg ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala 680 685 690	2179
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala 695 700 705	2227
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser 710 715 720 725	2275
acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser 730 735 740	2323
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp 745 750 755	2371
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly 760 765 770	2419
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr 775 780 785	2467
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe 790 795 800 805	2515
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu 810 815 820	2563
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala 825 830 835	2611
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys 840 845 850	2659
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro 855 860 865	2707

ctt ctc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc 2755
 Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu
 870 875 880 885

 aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa 2803
 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
 890 895 900

 agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc 2851
 Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
 905 910 915

 act gcg ctg cgc aac tcc ggc tagtccagcc ggctgggtag tac 2895
 Thr Ala Leu Arg Asn Ser Gly
 920

<210> 110
 <211> 924
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 110
 Val Phe Lys Val Val Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe
 1 5 10 15

 Leu Gly Gln Ile Leu Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu
 20 25 30

 Val Tyr Glu Leu Val Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala
 35 40 45

 Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
 50 55 60

 Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
 65 70 75 80

 Leu Leu Ala Asn Leu Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu
 85 90 95

 Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
 100 105 110

 Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
 115 120 125

 Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
 130 135 140

 Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr
 145 150 155 160

 Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
 165 170 175

 Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
 180 185 190

 Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
 195 200 205

Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu
 210 215 220
 Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg
 225 230 235 240
 Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly
 245 250 255
 Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu
 260 265 270
 Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr
 275 280 285
 Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp
 290 295 300
 Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly
 305 310 315 320
 His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val
 325 330 335
 His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
 340 345 350
 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
 355 360 365
 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
 370 375 380
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
 385 390 395 400
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
 405 410 415
 Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu
 420 425 430
 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
 435 440 445
 Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro
 450 455 460
 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile
 465 470 475 480
 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val
 485 490 495
 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu
 500 505 510
 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp
 515 520 525

Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu
 530 535 540

Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp
 545 550 555 560

Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met
 565 570 575

Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590

Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605

Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
 610 615 620

Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
 625 630 635 640

Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
 645 650 655

Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
 660 665 670

Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685

Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700

Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720

Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
 725 730 735

Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
 740 745 750

Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765

Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780

Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800

Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
 805 810 815

Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro
 820 825 830

Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr
 835 840 845

Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu

850	855	860
Leu Asp Asp Asn Pro	Leu Leu Ala Arg Ser Val	Gln Arg Arg Tyr Pro
865	870	875 880
Tyr Leu Leu Pro	Leu Asn Val Ile Gln Val	Glu Met Met Arg Arg Tyr
	885	890 895
Arg Lys Gly Asp	Gln Ser Glu Gln Val Ser Arg	Asn Ile Gln Leu Thr
	900	905 910
Met Asn Gly Leu Ser Thr	Ala Leu Arg Asn Ser Gly	
915	920	

<210> 111

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> RXN02326

<400> 111

ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60

ttcgaactca tcgaagacaa ctacgcaagc cgттаатgag	atg ctg gga cgc cca	115
	Met Leu Gly Arg Pro	
	1 5	

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac	163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His	
10 15 20	

ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa	211
Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln	
25 30 35	

aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt	259
Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu	
40 45 50	

ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg	307
Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu	
55 60 65	

gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa	355
Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu	
70 75 80 85	

gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc	403
Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser	
90 95 100	

ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac	451
Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His	
105 110 115	

cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc	499
---	-----

Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
 120 125 130
 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
 135 140 145
 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
 150 155 160 165
 aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
 170 175 180
 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
 185 190 195
 aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
 200 205 210
 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787
 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225
 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245
 tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
 250 255 260
 gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270
 ccc 939

<210> 112

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 112

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
 1 5 10 15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr

65	70	75	80
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys	85	90	95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu	100	105	110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp	115	120	125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile	130	135	140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile	145	150	155
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn	165	170	175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val	180	185	190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala	195	200	205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu	210	215	220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu	225	230	235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val	245	250	255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser	260	265	270

<210> 113

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA02326

<400> 113

ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60

ttcgaactca tcgaagacaa ctacgcaagc cgtaaatgag atg ctg gga cgc cca	115
Met Leu Gly Arg Pro	
1 5	

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac	163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His	

10							15							20							
ctc	gtt	ggt	gcg	ggt	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa	211					
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln						
			25					30					35								
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt	259					
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu						
		40					45					50									
ggt	aac	cct	cca	ggt	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg	307					
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu						
	55					60					65										
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa	355					
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu						
	70				75					80					85						
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc	403					
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser						
			90						95					100							
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac	451					
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His						
			105					110					115								
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc	499					
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe						
			120				125					130									
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547					
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val						
	135					140					145										
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595					
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp						
	150				155					160					165						
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca	643					
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro						
				170					175				180								
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa	691					
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu						
			185					190					195								
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt	739					
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly						
		200					205					210									
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat	787					
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp						
	215					220					225										
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835					
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala						
	230				235					240					245						
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883					
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys						
			250					255					260								

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270

ccc

939

<210> 114

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
 1 5 10 15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 195 200 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 210 215 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 225 230 235 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
 245 250 255

Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 260 265 270

<210> 115
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXN02327

<400> 115
 accgctgaag cagcttgccc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60

ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115
 Leu Leu Ala Thr Arg
 1 5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
200 205 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
215 220 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230 235 240 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
250 255 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
265 270 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
280 285 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
295 300 305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310 315 320

caa 1083

<210> 116

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
1 5 10 15

Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
20 25 30

Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
35 40 45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110
 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140
 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175
 Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190
 His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205
 Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220
 Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240
 Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255
 Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270
 Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285
 Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300
 Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 305 310 315 320

<210> 117

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> FRXA02327

<400> 117

```

accgctgaag cagcttggcc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60

ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115
                                   Leu Leu Ala Thr Arg
                                   1       5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
                                   10       15       20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
                                   25       30       35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
                                   40       45       50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
                                   55       60       65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
                                   70       75       80       85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
                                   90       95       100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
                                   105       110       115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
                                   120       125       130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
                                   135       140       145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
                                   150       155       160       165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
                                   170       175       180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
                                   185       190       195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739

```

Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
 200 205 210
 ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
 Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
 215 220 225
 ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
 Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
 230 235 240 245
 cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
 Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
 250 255 260
 tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
 Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
 265 270 275
 cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
 280 285 290
 ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
 Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
 295 300 305
 ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
 Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 310 315 320
 caa 1083

<210> 118
 <211> 320
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 118
 Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
 1 5 10 15
 Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
 20 25 30
 Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
 35 40 45
 Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 305 310 315 320

<210> 119
 <211> 1719
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1696)
 <223> RXN02328

<400> 119
 gaagtcgtgc aggtcagggg agtggtgccc gaaaacattg agaggaaaac aaaaaccgat 60

gtttgattgg gggaaatcggg gggtacgata ctaggacgca gtg act gct atc acc 115
 Val Thr Ala Ile Thr
 1 5

ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163

Leu	Gly	Gly	Leu	Leu	Leu	Lys	Gly	Ile	Ile	Thr	Leu	Val	Ser	Thr	His	
				10					15					20		
aca	tct	tca	acg	ctt	cca	gca	ttc	aaa	aag	atc	ttg	gta	gca	aac	cgc	211
Thr	Ser	Ser	Thr	Leu	Pro	Ala	Phe	Lys	Lys	Ile	Leu	Val	Ala	Asn	Arg	
			25					30					35			
ggc	gaa	atc	gcg	gtc	cgt	gct	ttc	cgt	gca	gca	ctc	gaa	acc	ggc	gca	259
Gly	Glu	Ile	Ala	Val	Arg	Ala	Phe	Arg	Ala	Ala	Leu	Glu	Thr	Gly	Ala	
		40					45					50				
gcc	acg	gta	gct	att	tac	ccc	cgt	gaa	gat	cgg	gga	tca	ttc	cac	cgc	307
Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly	Ser	Phe	His	Arg	
		55				60					65					
tct	ttt	gct	tct	gaa	gct	gtc	cgc	att	ggc	acc	gaa	ggc	tca	cca	gtc	355
Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu	Gly	Ser	Pro	Val	
70					75				80						85	
aag	gcg	tac	ctg	gac	atc	gat	gaa	att	atc	ggc	gca	gct	aaa	aaa	gtt	403
Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Gly	Ala	Ala	Lys	Lys	Val	
			90					95						100		
aaa	gca	gat	gcc	att	tac	ccg	gga	tac	ggc	ttc	ctg	tct	gaa	aat	gcc	451
Lys	Ala	Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	
			105				110							115		
cag	ctt	gcc	cgc	gag	tgt	gcg	gaa	aac	ggc	att	act	ttt	att	ggc	cca	499
Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro	
		120					125					130				
acc	cca	gag	gtt	ctt	gat	ctc	acc	ggc	gat	aag	tct	cgc	gcg	gta	acc	547
Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	
		135				140					145					
gcc	gcg	aag	aag	gct	ggc	ctg	cca	gtt	ttg	gcg	gaa	tcc	acc	ccg	agc	595
Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	
150				155				160						165		
aaa	aac	atc	gat	gag	atc	gtt	aaa	agc	gct	gaa	ggc	cag	act	tac	ccc	643
Lys	Asn	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	
			170					175						180		
atc	ttt	gtg	aag	gca	gtt	gcc	ggc	ggc	ggc	gga	cgc	ggc	atg	cgt	ttt	691
Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	
		185					190						195			
gtt	gct	tca	cct	gat	gag	ctt	cgc	aaa	tta	gca	aca	gaa	gca	tct	cgt	739
Val	Ala	Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	
		200					205					210				
gaa	gct	gaa	gcg	gct	ttc	ggc	gat	ggc	gcg	gta	tat	gtc	gaa	cgt	gct	787
Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	
	215					220					225					
gtg	att	aac	cct	cag	cat	att	gaa	gtg	cag	atc	ctt	ggc	gat	cac	act	835
Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	
230					235				240					245		
gga	gaa	gtt	gta	cac	ctt	tat	gaa	cgt	gac	tgc	tca	ctg	cag	cgt	cgt	883
Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	

250										255										260									
cac	caa	aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa														
His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu														
			265																										
ctg	cgt	gat	cg	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cg	tcc	att														
Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile														
			280																										
ggt	tac	cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc														
Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly														
			295																										
aac	cac	gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc														
Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr														
gtg	act	gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cg														
Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg														
ttg	gct	gct	gg	gca	acc	ttg	aag	gaa	ttg	gg	ctg	acc	caa	gat	aag														
Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys														
atc	aag	acc	cac	gg	gca	gca	ctg	cag	tgc	cg	atc	acc	acg	gaa	gat														
Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp														
cca	aac	aac	ggc	ttc	cg	cca	gat	acc	gga	act	atc	acc	gcg	tac	cg														
Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg														
tca	cca	ggc	gga	gct	ggc	gtt	cgt	ctt	gac	gg	gca	gct	cag	ctc	gg														
Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly														
ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	gtg	aaa	atg	acc	tgc														
Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys														
cgt	gg	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	gca	cag	cg	gcg	ttg														
Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu														
gct	gag	ttc	acc	gtg	tct	gg	gtt	gca	acc	aac	att	gg	ttc	ttg	cgt														
Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg														
gcg	ttg	ctg	cg	gaa	gag	gac	ttc	act	tcc	aag	cg	atc	gcc	acc	gga														
Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg	Ile	Ala	Thr	Gly														
ttc	att	gcc	gat	cac	ccg	cac	ctc	ctt	cag	gct	cca	cct	gct	gat	gat														
Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp														
gag	cag	gga	cg	atc	ctg	gat	tac	ttg	gca	gat	gtc	acc	gtg	aac	aag														
Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys														

cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg 1651
 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
 505 510 515

cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc 1696
 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 520 525 530

tgaagcagct tggcccagcc gcg 1719

<210> 120

<211> 532

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Val Thr Ala Ile Thr Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr
 1 5 10 15

Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
 20 25 30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
 35 40 45

Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
 50 55 60

Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 65 70 75 80

Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
 85 90 95

Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
 100 105 110

Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
 130 135 140

Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
 180 185 190

Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
 195 200 205

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile

225		230		235		240
Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys						
		245		250		255
Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln						
		260		265		270
His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys						
		275		280		285
Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu						
		290		295		300
Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile						
		305		310		315
Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val						
		325		330		335
Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly						
		340		345		350
Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg						
		355		360		365
Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr						
		370		375		380
Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly						
		385		390		395
Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu						
		405		410		415
Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg						
		420		425		430
Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn						
		435		440		445
Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys						
		450		455		460
Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala						
		465		470		475
Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp						
		485		490		495
Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala						
		500		505		510
Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly						
		515		520		525
Ser Arg Asp Arg						
		530				

<210> 121

<211> 1406
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1383)
 <223> FRXA02328

<400> 121

gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg	48
Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala	
1 5 10 15	
tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca	96
Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala	
20 25 30	
gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt	144
Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu	
35 40 45	
gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca	192
Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro	
50 55 60	
gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg	240
Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala	
65 70 75 80	
aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac	288
Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn	
85 90 95	
atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt	336
Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe	
100 105 110	
gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct	384
Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala	
115 120 125	
tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct	432
Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala	
130 135 140	
gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att	480
Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile	
145 150 155 160	
aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa	528
Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu	
165 170 175	
gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa	576
Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln	
180 185 190	
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt	624
Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg	
195 200 205	

gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac	672
Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr	
210 215 220	
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac	720
Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His	
225 230 235 240	
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act	768
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr	
245 250 255	
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct	816
Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala	
260 265 270	
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag	864
Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys	
275 280 285	
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac	912
Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn	
290 295 300	
aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca	960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro	
305 310 315 320	
ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa	1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu	
325 330 335	
atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt	1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly	
340 345 350	
tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag	1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu	
355 360 365	
ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg	1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu	
370 375 380	
ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att	1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile	
385 390 395 400	
gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag	1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln	
405 410 415	
gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat	1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His	
420 425 430	
ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac	1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn	
435 440 445	

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

tggtccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
 1 5 10 15

Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
 210 215 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
 225 230 235 240

Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
 245 250 255

Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
 260 265 270
 Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
 275 280 285
 Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
 290 295 300
 Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
 305 310 315 320
 Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
 325 330 335
 Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
 340 345 350
 Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
 355 360 365
 Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
 370 375 380
 Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

<210> 123

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN01048

<400> 123

agctacagat ttagctagtgt tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttccccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931

Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaaa cttgaggcccc aca 1347
 Pro Ile Phe

<210> 124

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
 370 375 380
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe

405

<210> 125
 <211> 311
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(288)
 <223> FRXA01048

<400> 125
 cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95
 taagagcaaa cttgaggccc aca 311

<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
85 90 95

```
<210> 127
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1063)  
<223> FRXA00290
```

<400> 127																
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca																60
gagcttcccg caaaaacacc gattaacaag gctaaatgat																115
Met Thr Ile Asp Leu																
1 5																
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac																163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His																
10 15 20																
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg																211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met																
25 30 35																
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa																259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu																
40 45 50																
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga																307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly																
55 60 65																
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc																355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly																
70 75 80 85																
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag																403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln																
90 95 100																
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac																451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp																
105 110 115																
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct																499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro																
120 125 130																
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc																547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe																
135 140 145																

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165
 gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180
 tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
 185 190 195
 tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
 Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
 200 205 210
 gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
 Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
 215 220 225
 gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
 Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
 230 235 240 245
 acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260
 gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275
 ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290
 acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305
 gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 128

<211> 321

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr

50 55 60
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 129
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1042)

<223> RXA02694

<400> 129

attaaagggtg taacaaagga atccggggcac aagctcttgc tgattttctg agctgctttg 60

tgggttgtcc ggtagggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115
 Met Lys Glu Thr Val
 1 5

ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
 Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
 10 15 20

gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
 Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
 25 30 35

gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
 Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
 40 45 50

ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
 Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr
 55 60 65

gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc 355
 Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala
 70 75 80 85

caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag 403
 Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys
 90 95 100

att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc 451
 Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly
 105 110 115

atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg 499
 Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val
 120 125 130

tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act 547
 Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr
 135 140 145

gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa 595
 Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu
 150 155 160 165

gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac 643
 Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp
 170 175 180

act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt 691
 Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu
 185 190 195

agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa 739
 Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys
 200 205 210

att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225

ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245

gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260

cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275

gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290

cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
 295 300 305

cag aag cag ttc ttc taaatctttg ggcgctagtt ggc 1065
 Gln Lys Gln Phe Phe
 310

<210> 130

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp
 1 5 10 15

Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp
 20 25 30

His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45

Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60

Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80

Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95

Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110

Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125

Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val

```
<210> 131
<211> 2967
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(2944)
<223> RXN00296
```

[illegible]

gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg	259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val	
40 45 50	
gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct	307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser	
55 60 65	
gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt	355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly	
70 75 80 85	
gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat	403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp	
90 95 100	
att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt	451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys	
105 110 115	
gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg	499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro	
120 125 130	
gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg gaa aat	595
Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
150 155 160 165	
ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg	643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac	691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
250 255 260	
ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg	931
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979

Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	Leu	Leu	
		280					285					290				
gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	aat	ctt	1027
Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	Asn	Leu	
		295				300					305					
cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tggttg	tac	tgc	gag		1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
310					315					320					325	
aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
				330					335						340	
gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
			345					350					355			
gaa	atg	cgg	gaa	ttg	tggtg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	att	gtc	1219
Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
		360					365					370				
acg	cgc	tta	gct	gat	gggtg	ggg	gaa	gcg	tggtg	ccg	aat	tggtg	gaa	gac	tcg	1267
Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
		375				380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggt	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
			425					430					435			
ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
		440					445					450				
gcg	tct	tat	ggt	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggt	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
		455				460					465					
cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tggtg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
			505					510					515			
ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	

520	525	530	
gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt gta tcc Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly Val Ser 535 540 545			1747
gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa atc acc Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln Ile Thr 550 555 560 565			1795
ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc tct gag Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu Ser Glu 570 575 580			1843
atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa gaa gtc Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu Glu Val 585 590 595			1891
aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca tcg gaa Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala Ser Glu 600 605 610			1939
tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc ctg gac Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe Leu Asp 615 620 625			1987
aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc atg ggc Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val Met Gly 630 635 640 645			2035
tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro 650 655 660			2083
acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca gtg gtg Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro Val Val 665 670 675			2131
cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His 680 685 690			2179
cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val 695 700 705			2227
gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala 710 715 720 725			2275
cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile 730 735 740			2323
cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln 745 750 755			2371
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys 760 765 770			2419

ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc 2467
 Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
 775 780 785

acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat 2515
 Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
 790 795 800 805

ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca 2563
 Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
 810 815 820

cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa 2611
 Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
 825 830 835

tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac 2659
 Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
 840 845 850

cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa 2707
 Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
 855 860 865

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
 870 875 880 885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
 890 895 900

ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc 2851
 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
 905 910 915

tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt 2899
 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
 920 925 930

gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
 Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln
 935 940 945

taacgatcat gcaacaggtg ctc 2967

<210> 132

<211> 948

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Thr His Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser
 1 5 10 15

Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
 20 25 30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala

35					40					45					
Glu	Pro	Glu	Asn	Val	Glu	Gln	Ile	Arg	Asp	Ala	Ile	Ala	Val	Ala	Val
50					55					60					
Ala	Arg	Gly	Trp	Ser	Val	Val	Gly	Arg	Gly	Gly	Gly	Ser	Ser	Val	Ala
65					70					75					80
Gly	Asn	Ala	Ile	Gly	Glu	Gly	Leu	Ile	Ile	Asp	Thr	Ser	Arg	Tyr	Phe
				85					90					95	
Asn	Arg	Ile	Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu
			100					105					110		
Pro	Gly	Val	Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly
		115					120						125		
Leu	Thr	Tyr	Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly
		130					135					140			
Gly	Met	Val	Ala	Asn	Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly
145				150					155					160	
Thr	Ala	Ala	Glu	Asn	Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly
				165					170					175	
Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn
			180					185					190		
Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys
		195					200					205			
Glu	Leu	Gly	Arg	Phe	Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr
		210					215					220			
Leu	Ala	His	Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile
225				230							235				240
Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val
				245					250					255	
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg
			260					265					270		
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met
		275					280					285			
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu
		290					295				300				
Ala	Gly	Gln	Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly
305				310							315				320
Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln
				325					330					335	
Ala	Ala	Glu	Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val
			340					345					350		
Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser
		355					360					365			

Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro
 370 375 380

Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
 385 390 395 400

Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
 405 410 415

Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
 420 425 430

Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
 435 440 445

Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
 450 455 460

Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
 465 470 475 480

Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
 485 490 495

Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
 500 505 510

Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525

His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540

Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
 545 550 555 560

Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
 565 570 575

Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590

Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605

Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
 610 615 620

Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
 625 630 635 640

His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655

Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
 660 665 670

Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
 675 680 685

```

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
690                               695                               700

Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
705                               710                               715                               720

Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
725                               730                               735

Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
740                               745                               750

His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
755                               760                               765

Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
770                               775                               780

Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
785                               790                               795                               800

Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
805                               810                               815

Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
820                               825                               830

Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
835                               840                               845

Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
850                               855                               860

Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
865                               870                               875                               880

Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
885                               890                               895

Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
900                               905                               910

Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
915                               920                               925

Gln Ala Thr His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn
930                               935                               940

Asn Met Ala Gln
945

```

<210> 133

<211> 2858

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (2835)

<223> FRXA00296

<400> 133

acc atc aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct	48
Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser	
1 5 10 15	
cgc gcg aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct	96
Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser	
20 25 30	
gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa	144
Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu	
35 40 45	
aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg	192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly	
50 55 60	
tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg	240
Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala	
65 70 75 80	
atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att	288
Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile	
85 90 95	
tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg	336
Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val	
100 105 110	
gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac	384
Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr	
115 120 125	
ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt	432
Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val	
130 135 140	
gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg	480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala	
145 150 155 160	
gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc	528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val	
165 170 175	
act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc	576
Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu	
180 185 190	
acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt	624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly	
195 200 205	
cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac	672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His	
210 215 220	
gac atg gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att	720
Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile	
225 230 235 240	

act cgg ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt	768
Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu	
245 250 255	
gct gtc ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc	816
Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala	
260 265 270	
aaa ttg cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat	864
Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp	
275 280 285	
ctc ctc gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag	912
Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln	
290 295 300	
aat ctt cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac	960
Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr	
305 310 315 320	
tgc gag aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag	1008
Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu	
325 330 335	
gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag	1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu	
340 345 350	
cct tct gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc	1104
Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly	
355 360 365	
att gtc acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa	1152
Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu	
370 375 380	
gac tcg gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt	1200
Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu	
385 390 395 400	
tat gcg ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac	1248
Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His	
405 410 415	
ttt gga gaa ggc tgc gtc cac gtt cgc atc agt ttt gat ttc tct acc	1296
Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr	
420 425 430	
aag gaa ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc	1344
Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr	
435 440 445	
ttg gtg gcg tct tat ggt ggc agc ctc tcg ggc gag cat gga gac ggt	1392
Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly	
450 455 460	
cgc gcc cgc tca tcc ttc ctt gac cgc atg tat tca gca gaa atg cgt	1440
Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg	
465 470 475 480	

gca ctc ttc gaa gaa ttc aag ctg att ttc gat ccc cag cgc atc ttc	1488
Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
485 490 495	
aat ccg gga gtg ttg gtc tgg gca gat cct gtc atg caa gga ctt cgc	1536
Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
500 505 510	
atg gac ccg ggc cag cgc gcc ctc gac atc acg ccc gta cac aaa ttc	1584
Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
515 520 525	
tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt	1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
530 535 540	
gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa	1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
545 550 555 560	
atc acc ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc	1728
Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
565 570 575	
tct gag atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa	1776
Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
580 585 590	
gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca	1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
595 600 605	
tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc	1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
610 615 620	
ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
625 630 635 640	
atg ggc tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt	1968
Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
645 650 655	
ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca	2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
660 665 670	
gtg gtg cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc	2064
Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
675 680 685	
gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
690 695 700	
acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga	2160
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
705 710 715 720	
cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208

Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val	
725	730 735
gtc atc cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc	2256
Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr	
740	745 750
ggc caa ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg	2304
Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val	
755	760 765
atg aaa ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct	2352
Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro	
770	775 780
tcg tgc acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac	2400
Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn	
785	790 795 800
cct gat ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc	2448
Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val	
805	810 815
atc gca cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta	2496
Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu	
820	825 830
aca gaa tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta	2544
Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu	
835	840 845
ggc gac cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa	2592
Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys	
850	855 860
gat gaa caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc	2640
Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly	
865	870 875 880
ttt gaa aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag	2688
Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu	
885	890 895
ctg ttc ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt	2736
Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly	
900	905 910
ttc tcc tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg	2784
Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr	
915	920 925
cac ctt gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca	2832
His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala	
930	935 940
caa taacgatcat gcaacaggtg ctc	2858
Gln	
945	

<210> 134

<211> 945

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser
 1 5 10 15

Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser
 20 25 30

Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
 35 40 45

Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
 50 55 60

Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
 65 70 75 80

Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
 85 90 95

Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
 100 105 110

Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
 115 120 125

Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
 130 135 140

Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
 145 150 155 160

Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
 165 170 175

Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
 180 185 190

Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
 195 200 205

Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
 210 215 220

Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
 225 230 235 240

Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
 245 250 255

Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
 260 265 270

Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
 275 280 285

Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
 290 295 300

Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
 305 310 315 320
 Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
 325 330 335
 Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
 340 345 350
 Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
 355 360 365
 Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
 370 375 380
 Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
 385 390 395 400
 Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
 405 410 415
 Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
 420 425 430
 Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
 435 440 445
 Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
 450 455 460
 Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
 465 470 475 480
 Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
 485 490 495
 Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
 500 505 510
 Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
 515 520 525
 Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
 530 535 540
 Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
 545 550 555 560
 Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
 565 570 575
 Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
 580 585 590
 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
 595 600 605
 Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
 610 615 620

Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
 625 630 635 640
 Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
 645 650 655
 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
 660 665 670
 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
 675 680 685
 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
 690 695 700
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
 705 710 715 720
 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
 725 730 735
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
 740 745 750
 Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
 755 760 765
 Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
 770 775 780
 Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
 785 790 795 800
 Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
 805 810 815
 Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
 820 825 830
 Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
 835 840 845
 Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
 850 855 860
 Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
 865 870 875 880
 Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
 885 890 895
 Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
 900 905 910
 Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
 915 920 925
 His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
 930 935 940
 Gln

945

<210> 135

<211> 1383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1360)

<223> RXA01901

<400> 135

```

gcatgttgcc ttctctctgt gatcgctcgt ttcttcatcc aacgcgtcgc gcaccaagag 60

aactaaaatc taagtaaaac ccctccgaaa ggaaccaccc atg gtg aaa cgt caa 115
                               Met Val Lys Arg Gln
                               1 5

ctg ccc aac ccc gca gaa cta ctc gaa ctc atg aag ttc aaa aag cca 163
Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro
          10          15          20

gag ctc aac ggc aag aaa cga cgc cta gac tcc gcg ctc acc atc tac 211
Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr
          25          30          35

gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac 259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Ala Phe Asp
          40          45          50

tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt 307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg
          55          60          65

gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca 355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala
          70          75          80          85

gaa cac gta gac acc acc acc caa atc ctg ggc gga acc tcc tcc atg 403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met
          90          95          100

cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa 451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu
          105          110          115

ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc 499
Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala Ala Gly Ile Pro Phe
          120          125          130

acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc 547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr
          135          140          145

aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc 595
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg
          150          155          160          165

gaa atc tcc tac ggc ctc gtc gaa cgc gca gcc aaa gca gga ttc gac 643

```

Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala Lys Ala Gly Phe Asp	
170 175 180	
acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc	691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg	
185 190 195	
gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc	739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr	
200 205 210	
gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc	787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr	
215 220 225	
acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg	835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser Thr Gly Gly Thr Val	
230 235 240 245	
ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac	883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp	
250 255 260	
ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt	931
Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly	
265 270 275	
gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac	979
Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp	
280 285 290	
ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca	1027
Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro	
295 300 305	
gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa	1075
Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu	
310 315 320 325	
cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc	1123
Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val	
330 335 340	
gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac	1171
Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr	
345 350 355	
ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc	1219
Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile	
360 365 370	
gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt	1267
Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val	
375 380 385	
tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag	1315
Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys	
390 395 400 405	
atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att	1360
Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile	

410

415

420

taaaagtttc tctccttagc tat

1383

<210> 136

<211> 420

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met	Val	Lys	Arg	Gln	Leu	Pro	Asn	Pro	Ala	Glu	Leu	Leu	Glu	Leu	Met
1				5					10					15	

Lys	Phe	Lys	Lys	Pro	Glu	Leu	Asn	Gly	Lys	Lys	Arg	Arg	Leu	Asp	Ser
			20					25					30		

Ala	Leu	Thr	Ile	Tyr	Asp	Leu	Arg	Lys	Ile	Ala	Lys	Arg	Arg	Thr	Pro
		35					40					45			

Ala	Ala	Ala	Phe	Asp	Tyr	Thr	Asp	Gly	Ala	Ala	Glu	Ala	Glu	Leu	Ser
	50					55					60				

Ile	Thr	Arg	Ala	Arg	Glu	Ala	Phe	Glu	Asn	Ile	Glu	Phe	His	Pro	Asp
65					70					75				80	

Ile	Leu	Lys	Pro	Ala	Glu	His	Val	Asp	Thr	Thr	Thr	Gln	Ile	Leu	Gly
				85					90					95	

Gly	Thr	Ser	Ser	Met	Pro	Phe	Gly	Ile	Ala	Pro	Thr	Gly	Phe	Thr	Arg
			100					105					110		

Leu	Met	Gln	Thr	Glu	Gly	Glu	Ile	Ala	Gly	Ala	Gly	Ala	Ala	Gly	Ala
		115					120					125			

Ala	Gly	Ile	Pro	Phe	Thr	Leu	Ser	Thr	Leu	Gly	Thr	Thr	Ser	Ile	Glu
	130					135					140				

Asp	Val	Lys	Ala	Thr	Asn	Pro	Asn	Gly	Arg	Asn	Trp	Phe	Gln	Leu	Tyr
145					150					155				160	

Val	Met	Arg	Asp	Arg	Glu	Ile	Ser	Tyr	Gly	Leu	Val	Glu	Arg	Ala	Ala
			165						170					175	

Lys	Ala	Gly	Phe	Asp	Thr	Leu	Met	Phe	Thr	Val	Asp	Thr	Pro	Ile	Ala
			180					185					190		

Gly	Tyr	Arg	Ile	Arg	Asp	Ser	Arg	Asn	Gly	Phe	Ser	Ile	Pro	Pro	Gln
		195				200						205			

Leu	Thr	Pro	Ser	Thr	Val	Leu	Asn	Ala	Ile	Pro	Arg	Pro	Trp	Trp	Trp
	210					215					220				

Ile	Asp	Phe	Leu	Thr	Thr	Pro	Thr	Leu	Glu	Phe	Ala	Ser	Leu	Ser	Ser
225					230					235				240	

Thr	Gly	Gly	Thr	Val	Gly	Asp	Leu	Leu	Asn	Ser	Ala	Met	Asp	Pro	Thr
				245					250					255	

Ile	Ser	Tyr	Glu	Asp	Leu	Lys	Val	Ile	Arg	Glu	Met	Trp	Pro	Gly	Lys
			260					265					270		

Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu
 275 280 285
 Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln
 290 295 300
 Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys
 305 310 315 320
 Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn
 325 330 335
 Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu
 340 345 350
 Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly
 355 360 365
 Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met
 370 375 380
 Ala Leu Leu Gly Val Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val
 385 390 395 400
 Thr Gln Leu Ala Lys Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala
 405 410 415
 Ala Ala Glu Ile
 420

<210> 137
 <211> 1836
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1813)
 <223> RXN01952

<400> 137
 ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60
 tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
 Met Thr Gln Pro Gly
 1 5
 cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
 Gln Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
 10 15 20
 gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
 25 30 35
 agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac	307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp	
55 60 65	
aac aac ctc atc gtc atc ccg cag gca tcc aac acg ggc ctg act ggt	355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly	
70 75 80 85	
gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc	403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile	
90 95 100	
tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag	451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu	
105 110 115	
gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc	499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu	
120 125 130	
gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc	547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile	
135 140 145	
ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag	595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
150 155 160 165	
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc	643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
170 175 180	
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
185 190 195	
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027

Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu	Pro	Ile	Ser	Gly	Glu	
295						300					305					
tac	atg	ggc	cgc	agt	gcc	ttc	gac	ttg	gcc	gag	aag	tac	ggc	aaa	gac	1075
Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp	
310					315					320					325	
acc	ttc	gtc	ttc	ctg	aag	ttc	atg	agt	cca	gcg	ctg	cag	acg	cgc	atg	1123
Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met	
				330					335					340		
ttc	tcg	ttc	aag	acg	tgg	gcc	aac	ggc	ttg	ttc	tcg	aag	att	ccc	ggc	1171
Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly	
			345					350					355			
att	ggt	ccg	acc	ttc	gcc	gac	acg	gta	tcg	caa	gcc	atg	ttc	agc	gtg	1219
Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val	
		360					365					370				
ctg	ccc	aac	cag	ctg	ccc	aag	cgc	atg	atg	gag	tac	cgc	aac	cgt	ttc	1267
Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe	
	375					380					385					
gag	cat	cac	ctg	ctg	ctc	acc	gtc	agc	gag	tcg	cag	aag	gcc	gcg	agc	1315
Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser	
390					395				400						405	
gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggt	gag	1363
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu	
				410					415					420		
ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg	
			425					430					435			
ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg	
		440					445					450				
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp	
	455					460					465					
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu	
470					475				480					485		
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp	
				490					495					500		
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile	
			505					510					515			
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn	
		520					525					530				
tac	ggt	cgc	atg	tac	aag	ctg	ccg	gag	tcc	atg	gaa	gag	cac	ttc	aag	1747
Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met	Glu	Glu	His	Phe	Lys	

535 540 545
 gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg 1795
 Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser
 550 555 560 565

 ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 1836
 Pro His Lys Asp Trp Ala
 570

 <210> 138
 <211> 571
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 138
 Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
 1 5 10 15

 Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30

 Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
 35 40 45

 Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60

 Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80

 Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95

 Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110

 Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125

 Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140

 Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

 Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175

 Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190

 Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205

 Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220

 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
 485 490 495
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
 500 505 510
 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
 515 520 525
 Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
 530 535 540
 Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly
 545 550 555 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala
565 570

```
<210> 139
<211> 239
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(216)  
<223> FRXA01952
```

<400> 139																
cca	gga	cta	tgt	cgc	caa	gca	ggg	cgt	gga	tct	caa	ggc	gct	gac	gac	48
Pro	Gly	Leu	Cys	Arg	Gln	Ala	Gly	Arg	Gly	Ser	Gln	Gly	Ala	Asp	Asp	
1				5				10						15		
cgc	atc	cag	cac	ttg	ctg	gag	gag	cac	ggc	aag	aag	ctg	ccc	gcc	gag	96
Arg	Ile	Gln	His	Leu	Leu	Glu	Glu	His	Gly	Lys	Lys	Leu	Pro	Ala	Glu	
			20					25					30			
cac	aac	tac	ggt	cgc	atg	tac	aag	ctg	ccg	gag	tcc	atg	gaa	gag	cac	144
His	Asn	Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met	Glu	Glu	His	
		35					40					45				
ttc	aag	gag	ctc	gat	ccg	acg	aat	acg	ttc	aac	gcc	ggt	atc	ggc	ggc	192
Phe	Lys	Glu	Leu	Asp	Pro	Thr	Asn	Thr	Phe	Asn	Ala	Gly	Ile	Gly	Gly	
	50					55					60					
acg	tcg	ccg	cac	aag	gac	tgg	gcc	taagtcccca				aggtagcgcg			acg	239
Thr	Ser	Pro	His	Lys	Asp	Trp	Ala									
65				70												

```
<210> 140
<211> 72
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 140
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
  1                               5          10                15

Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
                20                        25                30

His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
          35                        40                45

Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
  50                        55                60

Thr Ser Pro His Lys Asp Trp Ala
  65                70

```

<210>	141
<211>	1699
<212>	DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1699)

<223> FRXA01955

<400> 141

ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60

tgacgcgctt	gtgatgcaac	tgaatatagg	aagcttagag	atg	acg	caa	cca	gga	115
				Met	Thr	Gln	Pro	Gly	
				1				5	

cag	acc	acc	acg	act	tcg	cac	gaa	gcg	atc	gat	gcg	ttc	aag	aga	atc	163
Gln	Thr	Thr	Thr	Thr	Ser	His	Glu	Ala	Ile	Asp	Ala	Phe	Lys	Arg	Ile	
			10					15						20		

gtc	ggc	gac	gaa	cat	gta	ctg	acc	tct	gag	cgt	gcc	acg	atg	cca	ttc	211
Val	Gly	Asp	Glu	His	Val	Leu	Thr	Ser	Glu	Arg	Ala	Thr	Met	Pro	Phe	
			25					30					35			

agc	aaa	ggc	tat	cga	ttc	ggc	gga	gga	cca	gtc	ttc	gcc	gtg	gtg	cgc	259
Ser	Lys	Gly	Tyr	Arg	Phe	Gly	Gly	Gly	Pro	Val	Phe	Ala	Val	Val	Arg	
			40				45					50				

ccc	ggc	acg	ctg	gtc	gag	atg	tgg	cgg	gcg	ctg	cag	gta	tcc	gtc	gac	307
Pro	Gly	Thr	Leu	Val	Glu	Met	Trp	Arg	Ala	Leu	Gln	Val	Ser	Val	Asp	
	55					60					65					

aac	aac	ctc	atc	gtc	atc	ccg	cag	gca	tcg	aac	acg	ggc	ctg	act	ggt	355
Asn	Asn	Leu	Ile	Val	Ile	Pro	Gln	Ala	Ser	Asn	Thr	Gly	Leu	Thr	Gly	
70					75					80					85	

gga	tcc	ggc	ccc	ggc	ttc	caa	gac	tac	gat	cgc	ccc	att	gtg	atc	atc	403
Gly	Ser	Gly	Pro	Gly	Phe	Gln	Asp	Tyr	Asp	Arg	Pro	Ile	Val	Ile	Ile	
			90						95					100		

tcg	act	cac	cgc	atc	gat	gag	gtg	cac	ctc	atc	aac	gac	gcg	cgc	gag	451
Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile	Asn	Asp	Ala	Arg	Glu	
			105					110					115			

gcg	atc	tcg	ctc	gcg	ggc	acc	ccg	ctg	aca	cac	ctg	acc	gac	gcg	ctc	499
Ala	Ile	Ser	Leu	Ala	Gly	Thr	Pro	Leu	Thr	His	Leu	Thr	Asp	Ala	Leu	
		120					125					130				

gcc	aag	cac	cag	cgc	gag	ccg	cac	tcg	gtg	atc	ggg	tcg	aca	tca	atc	547
Ala	Lys	His	Gln	Arg	Glu	Pro	His	Ser	Val	Ile	Gly	Ser	Thr	Ser	Ile	
	135					140					145					

ggc	gcc	tcg	gtc	atc	ggc	ggc	atc	gcg	aac	aac	tcg	ggc	ggc	agc	cag	595
Gly	Ala	Ser	Val	Ile	Gly	Gly	Ile	Ala	Asn	Asn	Ser	Gly	Gly	Ser	Gln	
150					155					160					165	

att	cgc	aag	ggt	ccg	gca	ttc	acg	cgc	gaa	gcg	atc	ttc	gcc	cgc	gtc	643
Ile	Arg	Lys	Gly	Pro	Ala	Phe	Thr	Arg	Glu	Ala	Ile	Phe	Ala	Arg	Val	
			170					175					180			

aac	gac	gac	ggc	aag	gtc	gag	ctg	gtc	aat	cac	ctg	ggc	atc	tcg	ctc	691
Asn	Asp	Asp	Gly	Lys	Val	Glu	Leu	Val	Asn	His	Leu	Gly	Ile	Ser	Leu	
			185				190								195	

gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser	
390 395 400 405	
gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag	1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu	
410 415 420	
ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg	1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg	
425 430 435	

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450
 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465
 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485
 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500
 tat gtc gcc aag cag gcc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515
 cag cac ctg ctg gag gag cgc gcc gcg aag ctg ccc gcc gag cac aac 1699
 Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
 520 525 530

<210> 142
 <211> 533
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 142
 Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
 1 5 10 15
 Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30
 Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
 35 40 45
 Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60
 Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80
 Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95
 Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110
 Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125
 Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140
 Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175
 Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190
 Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205
 Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220
 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240
 Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His

[illegible]

```
<210> 143
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00293
```

<400> 143																
agagattggtt gattcgggcac caactttacc cacgagggta gaaatgaagc attcagggatg 60																
acaaaaaccca acctcacacc aacaacctat cctggagccc atg aaa atc ttt gtt 115																
Met Lys Ile Phe Val 5																
ggg 1																
ggt ttt ggc gat tat cca ctc acc acc aag gcc ctt aag gag gca ggc 163																
Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala Leu Lys Glu Ala Gly 20																
10 15																
gca gaa ata gtg gac tcc ctc gaa aaa gcc gag ggg ttt gtc ttc act 211																
Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu Gly Phe Val Phe Thr 35																
25 30																
caa aca cca ggc aca gaa ttt ccc cta ctt ccc gac gga gtg agg tgg 259																
Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro Asp Gly Val Arg Trp 50																
40 45																
gtg caa ttt ccc aat gcg ggg ctc aac gca tat ttc aca gct ggg cag 307																
Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr Phe Thr Ala Gly Gln 65																
55 60 65																
att gat gac aaa cgc cgg tgg tca aat gca tca ggg gtg tat ggc caa 355																
Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser Gly Val Tyr Gly Gln 85																
70 75 80																
cag gta gcc gaa gca gca atg gct ctt ttg ctg gga ctg att cat atg 403																
Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu Gly Leu Ile His Met 100																
90 95																
cac ccc acc atg gtg cgt gcc gat agt tgg gca cca agc act caa ata 451																
His Pro Thr Met Val Arg Ala Asp Ser Trp Ala Pro Ser Thr Gln Ile 115																
105 110																
gat cag cag acc aga tgg ctt gat ggt gca aca gtt gcc att gtg gga 499																
Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr Val Ala Ile Val Gly 120																
125 130																

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc 547
 Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
 135 140 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt 595
 Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
 150 155 160 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc 643
 Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
 170 175 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg 691
 Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
 185 190 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc 739
 Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
 200 205 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc 787
 Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
 215 220 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
 230 235 240 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
 250 255 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
 265 270 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
 280 285 290

atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 295 300

tag 1035

<210> 144

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Lys Ile Phe Val Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala
 1 5 10 15

Leu Lys Glu Ala Gly Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu
 20 25 30

Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro
 35 40 45

Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
 50 55 60
 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
 65 70 75 80
 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
 85 90 95
 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
 100 105 110
 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
 115 120 125
 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
 130 135 140
 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
 145 150 155 160
 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
 165 170 175
 Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
 180 185 190
 Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
 195 200 205
 Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
 210 215 220
 Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
 245 250 255
 Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
 260 265 270
 Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
 275 280 285
 Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 290 295 300

<210> 145

<211> 687

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (62)..(664)

<223> RXN01130

<400> 145

agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
195 200

tga 687

<210> 146

<211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 146

```

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1             5             10             15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20             25             30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35             40             45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50             55             60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65             70             75             80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85             90             95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100            105            110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115            120            125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130            135            140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145            150            155            160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165            170            175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180            185            190

Ala Thr Ser Phe Gln Val Asp Leu Asp
      195            200
  
```

<210> 147
 <211> 326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(303)
 <223> FRXA01130

<400> 147

```

gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc      48
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1             5             10             15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg      96
  
```

```

Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
      20                      25                      30

cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg   144
Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
      35                      40                      45

ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag   192
Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
      50                      55                      60

aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct   240
Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
      65                      70                      75                      80

gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc   288
Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
      85                      90                      95

cag gtt gat ctt gac taattagaga tccatttgct tga   326
Gln Val Asp Leu Asp
      100

```

<210> 148
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

```

<400> 148
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
  1                      5                      10                      15

Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
      20                      25                      30

Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
      35                      40                      45

Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
      50                      55                      60

Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
      65                      70                      75                      80

Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
      85                      90                      95

Gln Val Asp Leu Asp
      100

```

<210> 149
 <211> 604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> RXN03112

<400> 149

gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtagag ggcgagtgga agcgggtcttc tttcaacgggt gtg gaa att ttc gga 115
Val Glu Ile Phe Gly
1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
70 75 80 85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
90 95 100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
105 110 115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
120 125 130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
135 140 145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
150 155 160 165

gcg ctg gct 604
Ala Leu Ala

<210> 150

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
1 5 10 15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
 20 25 30
 Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
 35 40 45
 Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
 50 55 60
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
 65 70 75 80
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
 85 90 95
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160
 Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 151
 <211> 649
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(649)
 <223> FRXA01133

<400> 151
 tgtttctagt cgcacgccaa aaccggcggt ggacacgtct gcagccgacg cggtcgtgcc 60
 tgttgtagac ggacattcct agtttttcca ggagtaactt gtg agc cag aat ggc 115
 Val Ser Gln Asn Gly
 1 5
 cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163
 Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp
 10 15 20
 gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211
 Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg
 25 30 35
 cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt 259
 Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg
 40 45 50

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
 Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
 55 60 65
 aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
 Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
 70 75 80 85
 gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
 Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
 90 95 100
 att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
 Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
 105 110 115
 cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
 Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
 120 125 130
 ggt ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg 547
 Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
 135 140 145
 tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
 Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
 150 155 160 165
 ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
 Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
 170 175 180
 gcg ggt 649
 Ala Gly

<210> 152
 <211> 183
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 152
 Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
 1 5 10 15
 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60
 Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
 165 170 175

Leu Thr Leu Leu Arg Ala Gly
 180

<210> 153
 <211> 1011
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(988)
 <223> RXN00871

<400> 153
 gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacgggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451

Ala	Val	Ala	Glu	Ala	Pro	Thr	Gln	Glu	Pro	Lys	Glu	Trp	Lys	Tyr	Ile	
			105					110					115			
gct	cca	gca	gaa	act	cct	gtg	gag	ttg	cgt	gga	gct	ggc	cgc	tcg	agc	499
Ala	Pro	Ala	Glu	Thr	Pro	Val	Glu	Leu	Arg	Gly	Ala	Gly	Arg	Ser	Ser	
			120				125					130				
cga	caa	gtc	cac	aac	ttt	ggc	acc	ccg	gaa	gct	ctc	gat	gct	gct	cga	547
Arg	Gln	Val	His	Asn	Phe	Gly	Thr	Pro	Glu	Ala	Leu	Asp	Ala	Ala	Arg	
			135			140					145					
cta	atc	gtg	tgt	gaa	gta	atc	acc	cca	ggg	gaa	aac	tgg	agc	tct	tac	595
Leu	Ile	Val	Cys	Glu	Val	Ile	Thr	Pro	Gly	Glu	Asn	Trp	Ser	Ser	Tyr	
					155					160					165	
cct	cca	cac	aag	cat	gat	gag	cac	atc	cca	gga	cac	gag	tcc	aag	ctg	643
Pro	Pro	His	Lys	His	Asp	Glu	His	Ile	Pro	Gly	His	Glu	Ser	Lys	Leu	
				170					175					180		
gag	gaa	atc	tac	tac	ttc	gaa	agc	gcc	cca	tcg	cga	gtt	ggg	ggc	agg	691
Glu	Glu	Ile	Tyr	Tyr	Phe	Glu	Ser	Ala	Pro	Ser	Arg	Val	Gly	Gly	Arg	
			185					190					195			
gcc	gaa	gca	gca	gaa	gga	gct	ttc	gga	atg	ttt	tcc	acc	tac	tcc	tca	739
Ala	Glu	Ala	Ala	Glu	Gly	Ala	Phe	Gly	Met	Phe	Ser	Thr	Tyr	Ser	Ser	
			200				205					210				
cca	gcg	ggg	gag	atc	gat	atc	aac	gcc	atg	gtg	tac	agc	ggc	gat	atc	787
Pro	Ala	Gly	Glu	Ile	Asp	Ile	Asn	Ala	Met	Val	Tyr	Ser	Gly	Asp	Ile	
			215			220					225					
gcg	cta	gtt	cct	ttc	gga	tac	cac	ggc	cct	gcc	gtg	gca	gca	cct	ggc	835
Ala	Leu	Val	Pro	Phe	Gly	Tyr	His	Gly	Pro	Ala	Val	Ala	Ala	Pro	Gly	
					235					240					245	
tat	gac	ttg	tac	tac	ctc	aac	gtc	atg	gca	gga	cct	gat	ccg	gag	aga	883
Tyr	Asp	Leu	Tyr	Tyr	Leu	Asn	Val	Met	Ala	Gly	Pro	Asp	Pro	Glu	Arg	
				250					255					260		
atc	tgg	ctg	att	aac	gat	gac	cca	gcg	cac	gcc	tgg	gtt	cga	gat	aca	931
Ile	Trp	Leu	Ile	Asn	Asp	Asp	Pro	Ala	His	Ala	Trp	Val	Arg	Asp	Thr	
			265					270					275			
tgg	acc	ggg	caa	gca	ttt	gat	gat	cgc	ttg	cca	tat	gag	aac	gca	aac	979
Trp	Thr	Gly	Gln	Ala	Phe	Asp	Asp	Arg	Leu	Pro	Tyr	Glu	Asn	Ala	Asn	
			280				285					290				
aag	gag	gga	taaaatttca	tggtgaaac	gaa											1011
Lys	Glu	Gly														
			295													

<210> 154

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met	Arg	Trp	Phe	His	Lys	Lys	Gly	Glu	Leu	Ala	Arg	Asp	Gly	Trp	Gln	
1				5					10					15		

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

gggaaaaggc gatcaccagc cggttggtcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
 Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
 105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
 Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
 120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
 Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
 135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
 Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
 150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
 Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
 170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
 Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
 185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
 Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

200	205	210	
cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc			787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile			
215	220	225	
gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc			835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly			
230	235	240	245
tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga			883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg			
250	255		260
atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca			931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr			
265	270		275
tgg acc ggg caa gca ttt gat gat cgc ttg cca			964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro			
280	285		
<210> 156			
<211> 288			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 156			
Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln			
1	5	10	15
Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg			
20	25		30
Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly			
35	40		45
Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His			
50	55		60
His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly			
65	70	75	80
Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser			
85	90		95
Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys			
100	105		110
Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly			
115	120		125
Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala			
130	135		140
Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu			
145	150	155	160
Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly			
165	170		175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285

<210> 157
 <211> 373
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXN02829

<400> 157
 tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60
 ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5
 cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20
 tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35
 gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50
 gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65
 gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

70

75

80

85

gga cat atg acg tgg gat
 Gly His Met Thr Trp Asp
 90

373

<210> 158

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
 1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
 20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
 35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
 50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65 70 75 80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
 85 90

<210> 159

<211> 376

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(376)

<223> FRXA02829

<400> 159

tttttcgttt aatctcatat ttaaacacgt tccttttaaat tggttttata aattgataaa 60

ctgaattcgt cagtttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
 70 75 80 85

gga cat atg acg tgg gga tcc 376
 Gly His Met Thr Trp Gly Ser
 90

<210> 160

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
 1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
 20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
 35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
 50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65 70 75 80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
 85 90

<210> 161

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXN01468

<400> 161

tgccaaggat ttgaccacg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115
 Met Thr Val Asn Ile
 1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
 Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
 10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
 Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

25	30	35	
gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu 40 45 50			259
tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile 55 60 65			307
tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys 70 75 80 85			355
gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu 90 95 100			403
cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val 105 110 115			451
ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile 120 125 130			499
aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val 135 140 145			547
act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala 150 155 160 165			595
gca ctt att acc gca gct act ggc gct gag cct tat tac atc gcc aag Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys 170 175 180			643
cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His 185 190 195			691
tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys 200 205 210			739
tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile 215 220 225			787
tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val 230 235 240 245			835
atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly 250 255 260			883
gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp 265 270 275			925

tagtattctg taggtcatgg cat

948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
275

<210> 163

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> FRXA01468

<400> 163

```

tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60
ttagcgggaa aatttcgccc aaaacagggg caatgggtgtt atg aca gtg aac att 115
                                         Met Thr Val Asn Ile
                                         1           5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
              10              15              20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
              25              30              35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
              40              45              50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
              55              60              65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
              70              75              80              85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
              90              95              100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
              105              110              115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
              120              125              130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
              135              140              145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150              155              160              165

```

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180

cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195

tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210

tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225

tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245

atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260

gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275

tagtattctg taggtcatgg cat 948

<210> 164

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140
 Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160
 Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175
 Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190
 Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205
 Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220
 Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240
 Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255
 Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270
 Phe Thr Asp
 275

<210> 165
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA00794

<400> 165
 gcgggttgat acagcccaag cgccgataca ttataatgc gcctagatac gtgcaaccca 60
 cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
 Met Asn Leu Lys Asn
 1 5
 ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
 10 15 20
 gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
 25 30 35
 aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
 40 45 50
 tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
55						60					65						
gaa	gct	cca	atg	ctg	tac	aac	ggc	gaa	gag	gtc	gga	acc	ggc	ttt	gga	355	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
70					75					80					85		
cct	gag	gtt	gat	atc	gca	gtt	gac	cca	gtt	gac	ggc	acc	acc	ctg	atg	403	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95						100		
gct	gag	ggc	cgc	ccc	aac	gca	att	tcc	att	ctc	gca	gct	gca	gag	cgt	451	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Ala	Glu	Arg	
			105					110						115			
ggc	acc	atg	tac	gat	cca	tcc	tcc	gtc	ttc	tac	atg	aag	aag	atc	gcc	499	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
		120					125					130					
gtg	gga	cct	gag	gcc	gca	ggc	aag	atc	gac	atc	gaa	gct	cca	gtt	gcc	547	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
	135					140					145						
cac	aac	atc	aac	gcg	gtg	gca	aag	tcc	aag	gga	atc	aac	cct	tcc	gac	595	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
150				155						160					165		
gtc	acc	gtt	gtc	gtg	ctt	gac	cgt	cct	cgc	cac	atc	gaa	ctg	atc	gca	643	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac	att	cgt	cgt	gca	ggc	gca	aag	gtt	cgt	ctc	atc	tcc	gac	ggc	gac	691	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt	gca	ggc	gca	gtt	gca	gca	gct	cag	gat	tcc	aac	tcc	gtg	gac	atc	739	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
		200					205					210					
atg	atg	ggc	acc	ggc	gga	acc	cca	gaa	ggc	atc	atc	act	gcg	tgc	gcc	787	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
	215					220					225						
atg	aag	tgc	atg	ggc	ggc	gaa	atc	cag	ggc	atc	ctg	gcc	cca	atg	aac	835	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
230					235					240					245		
gat	ttc	gag	cgc	cag	aag	gca	cac	gac	gct	ggc	ctg	gtt	ctt	gat	cag	883	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255					260			
gtt	ctg	cac	acc	aac	gat	ctg	gtg	agc	tcc	gac	aac	tgc	tac	ttc	gtg	931	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
			265					270					275				
gca	acc	ggc	gtg	acc	aac	ggc	gac	atg	ctc	cgt	ggc	gtt	tcc	tac	cgc	979	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
		280					285					290					
gca	aac	ggc	gca	acc	acc	cgt	tcc	ctg	gtt	atg	cgc	gca	aag	tca	ggc	1027	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295 300 305
 acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
 310 315 320 325

 tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335

 aac 1128

 <210> 166
 <211> 335
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 166
 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
 1 5 10 15
 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
 20 25 30
 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
 35 40 45
 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
 50 55 60
 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
 65 70 75 80
 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
 85 90 95
 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
 100 105 110
 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
 115 120 125
 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
 130 135 140
 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
 145 150 155 160
 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
 165 170 175
 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
 180 185 190
 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
 195 200 205
 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
 210 215 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
 225 230 235 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
 245 250 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
 260 265 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
 275 280 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
 290 295 300

Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
 305 310 315 320

Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 325 330 335

<210> 167
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN02920

<400> 167
 tgc atg caga ttatctgtcc aactacgcc a g c g c g c g t a a a g c g c g g g c c t g c t g g t g g 60

cg g g t g g c g t c g a a a a g c a t t t t t a a a g g a g t t t a a g a c g a t g a a g t t t g t t a t g 115
 Met Lys Phe Val Met
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

	90	95	100	
gcg acg act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa	451			
Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu				
105 110 115				
aac aac aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc	499			
Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly				
120 125 130				
gcc ggt ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac	547			
Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn				
135 140 145				
gtg aag acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca	595			
Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala				
150 155 160 165				
gat gaa acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct	643			
Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala				
170 175 180				
gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc	691			
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile				
185 190 195				
gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc	739			
Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val				
200 205 210				
aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca	787			
Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala				
215 220 225				
ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct	835			
Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro				
230 235 240 245				
gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt	883			
Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val				
250 255 260				
atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc	931			
Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr				
265 270 275				
ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag	979			
Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln				
280 285 290				
atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat	1032			
Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr				
295 300				
ccg				1035

<210> 168

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
 1 5 10 15
 Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
 20 25 30
 Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
 35 40 45
 Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50 55 60
 Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65 70 75 80
 Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
 85 90 95
 Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
 100 105 110
 Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
 115 120 125
 Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
 130 135 140
 Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
 145 150 155 160
 Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
 165 170 175
 Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
 180 185 190
 Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
 195 200 205
 Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
 210 215 220
 Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
 245 250 255
 Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
 260 265 270
 Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
 275 280 285
 Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 290 295 300

```
<210> 169
<211> 779
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (52) .. (756)  
<223> FRXA02379
```

<400> 169

tg	cagg	cctc	cat	ggc	gggt	att	gat	gcgc	tggt	caag	cgc	tggt	gtc	gtc	aatg	aga	57
															Met	Arg	
															1		
aag	cac	cgt	tgg	gca	aac	gcg	gct	ggc	ctg	tac	gct	gac	acc	gtt	gct		105
Lys	His	Arg	Trp	Ala	Asn	Ala	Ala	Gly	Leu	Tyr	Ala	Asp	Thr	Val	Ala		
		5						10				15					
gag	tcc	acc	att	ggg	tta	att	ctg	gcg	cag	atg	cac	atg	cat	gcg	acg		153
Glu	Ser	Thr	Ile	Gly	Leu	Ile	Leu	Ala	Gln	Met	His	Met	His	Ala	Thr		
	20					25					30						
act	cgt	ttg	gct	aag	tcg	tgg	agc	gtg	cgg	cct	gag	gtg	gaa	aac	aac		201
Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu	Asn	Asn		
	35				40					45					50		
aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	gcc	ggt		249
Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly	Ala	Gly		
				55					60					65			
ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	gtg	aag		297
Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn	Val	Lys		
			70					75					80				
acc	att	gcg	gtt	aat	aac	tct	ggg	cgt	ccg	gtg	gaa	ggg	gca	gat	gaa		345
Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala	Asp	Glu		
		85					90					95					
acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	gat	gtg		393
Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala	Asp	Val		
	100					105					110						
ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	gtc	aat		441
Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile	Val	Asn		
115					120					125					130		
gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	aat	gtg		489
Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val	Asn	Val		
				135				140						145			
ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	ttg	aac		537
Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala	Leu	Asn		
			150					155					160				
aac	ggc	acc	att	gcg	ggg	gct	gcg	ctg	gac	gtt	acc	gat	cct	gag	cca		585
Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro	Glu	Pro		
		165				170						175					

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
 180 185 190

cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
 195 200 205 210

ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
 215 220 225

acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776
 Thr Glu Val Asp Val Val Ala Gly Tyr
 230 235

ccg 779

<210> 170

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 1 5 10 15

Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
 20 25 30

Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45

Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60

Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80

Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95

Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110

Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125

Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140

Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160

Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175

Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205

Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220

Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXN02688

<400> 171

gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc gcc cgg att 115
 Met Ala Gly Arg Ile
 1 5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg gcc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc gcc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100

ttt gaa atg cgc gcc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115

ctc aac gcc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc gcc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135 140 145
 atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc 595
 Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
 150 155 160 165
 agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg 643
 Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
 170 175 180
 gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
 Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
 185 190 195
 gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc 739
 Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
 200 205 210
 tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg 789
 Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
 215 220
 gat 792

 <210> 172
 <211> 223
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 172
 Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
 1 5 10 15
 Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
 20 25 30
 Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
 35 40 45
 Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
 50 55 60
 Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65 70 75 80
 Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
 85 90 95
 Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
 100 105 110
 Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
 115 120 125
 Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
 130 135 140
 Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
 145 150 155 160

Asp	Val	Ala	Val	Val	Ser	His	Gly	Ala	Val	Ile	Arg	Ile	Val	Ala	Thr
				165					170					175	
His	Ala	Thr	Gly	Val	Asp	Pro	Asn	Phe	Ala	Phe	Asn	Thr	Tyr	Leu	Gly
			180					185					190		
Asn	Cys	Arg	Phe	Val	Val	Leu	Glu	Pro	Asn	Gly	Lys	Lys	Phe	Ser	Gln
		195					200					205			
Trp	Asp	Val	Val	Arg	Trp	Thr	Asp	Ser	Pro	Leu	Pro	Trp	Gln	Glu	
	210					215					220				

```
<210> 173
<211> 336
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(313)
<223> RXN03087
```

<400> 173																
gttgccgcca gccgttccag ggcgcttgag ctggtcagcg acatcgcaat gatcaaccag																60
gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca																115
Met Lys Ile Tyr Ala																
1 5																
cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg																163
Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val																
10 15 20																
gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca																211
Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala																
25 30 35																
cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat																259
Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp																
40 45 50																
gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca																307
Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala																
55 60 65																
aag aac taatgggtca aaccgcgcatc att																336
Lys Asn																
70																

```
<210> 174
<211> 71
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 174
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
1 5 10 15
Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr

20 25 30

Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
35 40 45

Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
50 55 60

Leu Glu Leu Glu Ala Lys Asn
65 70

<210> 175
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> RXN03186

<400> 175
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
55 60 65

cgc 310
Arg
70

<210> 176
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
1 5 10 15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg
 65 70

<210> 177

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

ggt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

caagggacag ata 302

<210> 178

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

<210> 179

<211> 1953

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1930)

<223> RXN02591

<400> 179

atgtgtccgt tgtctcacct aaagtttttaa ctagttctgt atctgaaagc tacgctaggg 60

ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115
 Met Thr Thr Ala Ala
 1 5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163
 Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
 10 15 20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211
 Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
 25 30 35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259
 Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
 40 45 50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307
 Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
 55 60 65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355
 Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
 70 75 80 85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403
 Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
 90 95 100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451
 Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
 105 110 115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg 499
 Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
 120 125 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg 375 380 385	1267
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn 390 395 400 405	1315
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg 410 415 420	1363
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly 425 430 435	1411
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala 440 445 450	1459
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro 455 460 465	1507
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met 470 475 480 485	1555
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp 490 495 500	1603
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp 505 510 515	1651
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val 520 525 530	1699
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu 535 540 545	1747
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu 550 555 560 565	1795
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu 570 575 580	1843
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln 585 590 595	1891
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala 600 605 610	1940
gcttaagaac tgc	1953

<210> 180
 <211> 610
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180

```

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
 1           5           10           15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
      20           25           30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
      35           40           45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
      50           55           60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
      65           70           75           80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
      85           90           95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
      100          105          110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
      115          120          125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
      130          135          140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
      145          150          155          160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
      165          170          175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
      180          185          190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
      195          200          205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
      210          215          220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
      225          230          235          240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
      245          250          255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
      260          265          270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
      275          280          285

```

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
 325 330 335
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
 340 345 350
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
 355 360 365
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
 370 375 380
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
 385 390 395 400
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
 405 410 415
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
 420 425 430
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
 435 440 445
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
 450 455 460
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
 465 470 475 480
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
 485 490 495
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
 500 505 510
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
 515 520 525
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
 530 535 540
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
 545 550 555 560
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
 565 570 575
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
 580 585 590
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
 595 600 605

His Ala
610

<210> 181
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXS01260

<400> 181

```

ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgccatac 60

ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
                               Val Thr Phe Asn Tyr
                               1           5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
                10                15                20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
                25                30                35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
                40                45                50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
                55                60                65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
                70                75                80                85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
                90                95                100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
                105                110                115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
                120                125                130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
                135                140                145

aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
                150                155                160                165

```


gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctgcttggtgcc ctg	1305
His Met Ile Asn Phe	
390	

<210> 182
 <211> 394
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 182

Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser
1				5					10					15	
Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile
			20					25					30		
Ile	Glu	Ile	His	Gly	Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu
		35					40					45			
Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys
	50					55					60				
Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe
65					70					75					80
Ser	Glu	Asn	Val	Val	Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala
			85						90					95	
Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe
			100					105					110		
Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe
		115					120					125			
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile
	130					135					140				
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala
145					150					155					160
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln
			165						170					175	
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met
			180					185					190		
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225				230						235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
			245					250						255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
		260						265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val

290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
385 390

<210> 183
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXS01261

<400> 183
gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60
atgcacgaca atgacccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
Val Thr Glu His Tyr
1 5
gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
10 15 20
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
25 30 35
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
40 45 50
gat caa aaa cgc tgaagttgcc cataccttta ccc 294
Asp Gln Lys Arg
55

<210> 184
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 185
 <211> 1650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXA02640

<400> 185
 accaacgacg acgccggtgt agcagatgta ttggagtggt gggttctaata ggtggtgtta 60
 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
 Met Arg Ile Ser Lys
 1 5
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
 10 15 20
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
 25 30 35
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
 40 45 50
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
 55 60 65
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
 70 75 80 85
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
 90 95 100
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
 120 125 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
 375 380 385

cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
 390 395 400 405

gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
 410 415 420

ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
 425 430 435

ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
 440 445 450

ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
 455 460 465

gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
 470 475 480 485

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
 Val Glu His Ser Tyr Asp Gln Ala
 505

<210> 186

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly
 1 5 10 15

Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val
 20 25 30

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
 35 40 45

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
 50 55 60

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65 70 75 80

Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
 85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 245 250 255
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 260 265 270
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 275 280 285
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 290 295 300
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 305 310 315 320
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 325 330 335
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 340 345 350
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 355 360 365
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 370 375 380
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
 385 390 395 400
 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
 405 410 415
 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

420	425	430
Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val		
435	440	445
Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly		
450	455	460
Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys		
465	470	475
Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala		
485	490	495
Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala		
500	505	

<210> 187
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXN01025

<400> 187
 gggcagcagc ggcaggtttc caggaggttt ccatgcgggt ggcttgggac atgggctaac 60
 ctgagacggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115
 Val Val Ser Val Ser
 1 5
 gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20
 gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
 25 30 35
 agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
 40 45 50
 acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
 Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
 55 60 65
 gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
 70 75 80 85
 ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
 90 95 100
 gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser

105	110	115	
gaa gtg atc gcg gag gtg acg Glu Val Ile Ala Glu Val Thr 120	gaa gcg gat cct tca cgc Glu Ala Asp Pro Ser Arg 125	atc gcg gtg Ile Ala Val 130	499
ttg tcg ggg cca aac ctt gct Leu Ser Gly Pro Asn Leu 135	cgt gag atc gcg gag ggg Ala Arg Glu Ile Ala Glu 140	cag cct gca Gln Pro Ala 145	547
gct acg gtg att gct tgc cct Ala Thr Val Ile Ala Cys 150	gat gaa aac cga gcg aaa Pro Asp Glu Asn Arg Ala 155	ctt gtg cag Leu Val Gln 165	595
gct gca gtg gct gcg ccg tat Ala Ala Val Ala Ala Pro 170	ttc cgc ccg tac acc aac Tyr Phe Arg Pro Tyr Thr 175	act gat gtg Asn Thr Asp Val 180	643
gtg ggc act gaa atc ggt ggt Val Gly Thr Glu Ile Gly 185	gcg tgt aag aac gtc atc Ala Cys Lys Asn Val Ile 190	gcg ctg gcc Ala Leu Ala 195	691
tgt ggt att tcc cat ggt tac Cys Gly Ile Ser His Gly 200	ggc ctg ggt gag aac acc Gly Leu Gly Glu Asn Thr 205	aat gca tcg Asn Ala Ser 210	739
ttg att act cgt ggc ctt gca Leu Ile Thr Arg Gly Leu 215	gag atc gca cgc ctc ggt Ala Glu Ile Ala Arg Leu 220	gcc aca ttg Ala Thr Leu 225	787
ggt gcg gat gcg aag act ttt Gly Ala Asp Ala Lys Thr 230	tct ggc ctt gcg gga atg Ser Gly Leu Ala Gly Met 235	ggc gac ttg Gly Asp Leu 245	835
gtg gct acg tgt tca tca ccg Val Ala Thr Cys Ser Ser 250	ctg tcg cgt aac cgc agc Leu Ser Arg Asn Arg Ser 255	ttc ggt gag Phe Gly Glu 260	883
cgt ttg ggt cag ggt gaa tcc Arg Leu Gly Gln Gly Glu 265	cta gag aag gct cgc gag Leu Glu Lys Ala Arg Glu 270	gca acc aat Ala Thr Asn 275	931
ggt cag gtt gcg gag ggt gtt Gly Gln Val Ala Glu Gly 280	att tcc tcg cag tcg att Ile Ser Ser Gln Ser Ile 285	ttt gat ctt Phe Asp Leu 290	979
gcc acc aag ctt ggt gtg gag Ala Thr Lys Leu Gly Val 295	atg ccg atc acc cag gct Glu Met Pro Ile Thr Gln 300	gtc tac ggt Ala Val Tyr Gly 305	1027
gtg tgc cac cga gat atg aaa Val Cys His Arg Asp Met 310	gta act gac atg att gtg Val Thr Asp Met Ile Val 315	gct ctc atg Ala Leu Met 325	1075
ggc agg tct aag aag gct gag Gly Arg Ser Lys Lys Ala 330	tagtcttagg ttgtaagctt Glu	caa	1119

<210> 188

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
 1 5 10 15
 Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
 305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
 325 330

<210> 189
 <211> 1015
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1015)
 <223> FRXA01025

<400> 189
 gggcagcagc ggcaggtttc cagraggttt ccatgcgggt ggcttggrac wtgggctaac 60
 ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115
 Val Val Ser Val Ser
 1 5
 gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20
 gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
 25 30 35
 agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
 40 45 50
 acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
 Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
 55 60 65
 gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
 70 75 80 85
 ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
 90 95 100
 gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg ccg atg agt 451
 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
 105 110 115
 gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
 Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
 120 125 130
 ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
 Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
 135 140 145
 gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

Ala Thr Val Ile	Ala Cys Pro Asp Glu Asn Arg	Ala Lys Leu Val	Gln	
150	155	160	165	
gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg				643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val				
	170	175	180	
gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc				691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala				
	185	190	195	
tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg				739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser				
	200	205	210	
ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg				787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu				
	215	220	225	
ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg				835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu				
	230	235	240	245
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag				883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu				
	250	255	260	
cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat				931
Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn				
	265	270	275	
ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt				979
Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu				
	280	285	290	
gcc acc aag ctt ggt gtg gag atg ccg atc acc cag				1015
Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln				
	295	300	305	
<210> 190				
<211> 305				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 190				
Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu				
1	5	10	15	
Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg				
	20	25	30	
Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp				
	35	40	45	
Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser				
	50	55	60	
Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro				
	65	70	75	80

[illegible]

```
<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1786)
<223> RXA01851
```

```
<400> 191
ttgtggcctt tttgcagggg aaacttattt aaataattca taagtaaaaa accgtcaatt 60
cacgatgtgg gttggcgggtt ttccctattag gctcactttt atg acg agc gca cac    115
                               Met Thr Ser Ala His
```

1															5				
ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc	163																		
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val																			
10					15					20									
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct	211																		
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala																			
25					30					35									
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct	259																		
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser																			
40					45					50									
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc	307																		
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg																			
55					60					65									
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa	355																		
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu																			
70					75					80					85				
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt	403																		
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser																			
90					95					100									
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg	451																		
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu																			
105					110					115									
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag	499																		
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln																			
120					125					130									
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa	547																		
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys																			
135					140					145									
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag	595																		
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys																			
150					155					160					165				
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc	643																		
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu																			
170					175					180									
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc	691																		
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile																			
185					190					195									
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc	739																		
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg																			
200					205					210									
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag	787																		
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu																			
215					220					225									
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag	835																		
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln																			
230					235					240					245				

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc	883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser	
250 255 260	
aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg	931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val	
265 270 275	
ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg	979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met	
280 285 290	
ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct	1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala	
295 300 305	
gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc	1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr	
310 315 320 325	
atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc	1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser	
330 335 340	
acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac	1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr	
345 350 355	
acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att	1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile	
360 365 370	
gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg	1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val	
375 380 385	
atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg	1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val	
390 395 400 405	
tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act	1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr	
410 415 420	
tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt	1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu	
425 430 435	
cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg	1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu	
440 445 450	
gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca	1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala	
455 460 465	
aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc	1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile	
470 475 480 485	

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

tcatcgacac cgg 1809

<210> 192
 <211> 562
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
 Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
 1 5 10 15

Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
 165 170 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
 180 185 190
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
 195 200 205
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
 210 215 220
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
 225 230 235 240
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
 245 250 255
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
 260 265 270
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
 275 280 285
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
 290 295 300
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
 305 310 315 320
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495

[illegible]

```
<210> 193
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(877)  
<223> RXA01242
```

<400> 193																
cgccgggaac	caa	atg	agg	gc	tttt	ggg	cgt	tgg	acag	tga	gaca	atgg	ggt	aaga	aattcg	60
gacatatttta gtaaattggc tttttgcttt aaggagtgac																
											atg	tac	gca	gag	gag	115
											Met	Tyr	Ala	Glu	Glu	
											1				5	
cg	cgt	cga	cag	att	gcc	tca	tta	acg	gca	gtt	gag	gga	cgt	gta	aat	163
Arg	Arg	Arg	Gln	Ile	Ala	Ser	Leu	Thr	Ala	Val	Glu	Gly	Arg	Val	Asn	
				10					15					20		
gtc	aca	gaa	tta	gcg	ggc	cga	ttc	gat	gtc	act	gca	gag	acg	att	cga	211
Val	Thr	Glu	Leu	Ala	Gly	Arg	Phe	Asp	Val	Thr	Ala	Glu	Thr	Ile	Arg	
			25				30				35					
cga	gac	ctt	gcg	gtg	cta	gac	cgc	gag	gga	att	gtt	cac	cgc	gtt	cac	259
Arg	Asp	Leu	Ala	Val	Leu	Asp	Arg	Glu	Gly	Ile	Val	His	Arg	Val	His	
		40					45					50				
ggt	ggc	gca	gta	gcc	acc	caa	tct	ttc	caa	acc	aca	gag	ttg	agc	ttg	307
Gly	Gly	Ala	Val	Ala	Thr	Gln	Ser	Phe	Gln	Thr	Thr	Glu	Leu	Ser	Leu	
		55					60					65				
gat	act	cgt	ttc	agg	tct	gca	tcg	tca	gca	aag	tac	tc	att	gcc	aag	355
Asp	Thr	Arg	Phe	Arg	Ser	Ala	Ser	Ser	Ala	Lys	Tyr	Ser	Ile	Ala	Lys	
		70					75					80			85	
gca	gcg	atg	cag	ttc	ctg	ccc	gct	gag	cat	ggc	gga	ctg	ttc	ctc	gat	403
Ala	Ala	Met	Gln	Phe	Leu	Pro	Ala	Glu	His	Gly	Gly	Leu	Phe	Leu	Asp	
				90					95					100		
gcg	gga	act	act	gtt	act	gct	ttg	gcc	gat	ctc	att	tct	gag	cat	cct	451
Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu	Ile	Ser	Glu	His	Pro	
			105				110				115					

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
 120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
 135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
 150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
 170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
 185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
 250 255

tgattctttac agtcactgca agt 900

<210> 194

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
1 5 10 15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

85										90					95				
Gly	Leu	Phe	Leu	Asp	Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu				
			100						105				110						
Ile	Ser	Glu	His	Pro	Ser	Ser	Lys	Gln	Trp	Ser	Ile	Val	Thr	Asn	Cys				
		115					120					125							
Leu	Pro	Ile	Ala	Leu	Asn	Leu	Ala	Asn	Ala	Gly	Leu	Asp	Asp	Val	Gln				
	130					135					140								
Leu	Leu	Gly	Gly	Ser	Val	Arg	Ala	Ile	Thr	Gln	Ala	Val	Val	Gly	Asp				
145					150					155					160				
Thr	Ala	Leu	Arg	Thr	Leu	Ala	Leu	Met	Arg	Ala	Asp	Val	Val	Phe	Ile				
			165					170						175					
Gly	Thr	Asn	Ala	Leu	Thr	Leu	Asp	His	Gly	Leu	Ser	Thr	Ala	Asp	Ser				
		180					185						190						
Gln	Glu	Ala	Ala	Met	Lys	Ser	Ala	Met	Ile	Thr	Asn	Ala	His	Lys	Val				
	195					200						205							
Val	Val	Leu	Cys	Asp	Ser	Thr	Lys	Met	Gly	Thr	Asp	Tyr	Leu	Val	Ser				
	210					215					220								
Phe	Gly	Ala	Ile	Ser	Asp	Ile	Asp	Val	Val	Val	Thr	Asp	Ala	Gly	Ala				
225				230					235						240				
Pro	Ala	Ser	Phe	Val	Glu	Gln	Leu	Arg	Glu	Arg	Asp	Val	Glu	Val	Val				
			245					250					255						

Ile Ala Glu

<210> 195
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(946)
 <223> RXA02288

<400> 195
 aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatggttagaa 60
 agtgctggat ctaacaacat ttccgtggta actttttcac atg tcc caa gtg att 115
 Met Ser Gln Val Ile
 1 5
 ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
 10 15 20
 acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
 25 30 35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp	
40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser	
55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val	
70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala	
90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys	
105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr	
120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile	
135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys	
150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val	
170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His	
185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly	
200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly	
215 220 225	
gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat	835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp	
230 235 240 245	
cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg	883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala	
250 255 260	
cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca	931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro	
265 270 275	
acg gaa gag gat ttt taagatggct ttggttcttg gaa	969

Thr Glu Glu Asp Phe
280

<210> 196

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
1 5 10 15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 197
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> RXN01891

<400> 197
ggt ggc cac tat ggt ttg cct ttc gct cgc tcc act gtc ctc ttc tac 48
Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
1 5 10 15
tac aac aag gat ctg tgg got aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30
gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45
atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60
tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80
gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95
gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110
gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125
tcc acc ggt gat ctg tct tct gtt gcc ggc gct gca agc ttc gac tgg 432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ser Phe Asp Trp
130 135 140
ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160
ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
165 170 175
gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act 576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr

180	185	190	
ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct			624
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala			
195	200	205	
gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac			672
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr			
210	215	220	
aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc			720
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe			
225	230	235	240
cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag			768
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu			
245	250	255	
aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt			816
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val			
260	265	270	
gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att			864
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile			
275	280	285	
taatccgagc acttcagcta cac			887

<210> 198

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr			
1	5	10	15
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro			
20	25	30	
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala			
35	40	45	
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu			
50	55	60	
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser			
65	70	75	80
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val			
85	90	95	
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr			
100	105	110	
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln			
115	120	125	
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp			
130	135	140	

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160

Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
165 170 175

Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
180 185 190

Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
195 200 205

Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
210 215 220

Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
225 230 235 240

Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
245 250 255

Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
260 265 270

Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
275 280 285

<210> 199

<211> 842

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(819)

<223> FRXA01891

<400> 199

tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc 48
Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
1 5 10 15

cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
20 25 30

gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
35 40 45

ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
50 55 60

tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

65	70	75	80	
gtt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc				288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tct gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
gtt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

<210> 200

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
 180 185 190
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
 195 200 205
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
 210 215 220
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
 225 230 235 240
 Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
 245 250 255
 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
 260 265 270

Ile

<210> 201

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

```

tttaccatg agt tac aac agc ccg tat aac aac acg aat ttc agc acc act 51
  Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
    1             5             10             15

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
          20             25             30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
          35             40             45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
          50             55             60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
          65             70             75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
          80             85             90             95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
          100             105             110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
          115             120             125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
          130             135             140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
          145             150             155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
          160             165             170             175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
          180             185             190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
          195             200             205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
          210             215             220

```

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagcgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202
 <211> 249
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 202
 Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
 1 5 10 15
 Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
 20 25 30
 Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45
 Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60
 Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
 65 70 75 80
 Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
 85 90 95
 Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
 100 105 110
 Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
 115 120 125
 Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
 130 135 140
 Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
 145 150 155 160
 Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
 165 170 175
 Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
 180 185 190
 Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
 195 200 205
 His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
 210 215 220
 Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
 225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

<210> 203

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN01580

<400> 203

```

cggtaaacgc ctcattaaag tccaatgcc a tgctcataac actaacagtt aaccgtgcgg 60

tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
                               Met Tyr Lys Asn Met
                               1       5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
                10                15                20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
                25                30                35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
                40                45                50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
                55                60                65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
                70                75                80                85

tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
                90                95                100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
                105                110                115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
                120                125                130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
                135                140                145

cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150                155                160                165

```

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643
 Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
 170 175 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691
 Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
 185 190 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739
 Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
 200 205 210

caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787
 Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
 215 220 225

gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837
 Ala Pro Ser Pro Ala Gly Glu Leu His Trp
 230 235

ctg 840

<210> 204

<211> 239

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 204

Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
 1 5 10 15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
 20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
 35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
 50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
 85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
 100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
 115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
 130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

165								170				175			
Leu	Pro	Ser	Trp	Lys	Ala	Leu	Asn	Val	Ala	Ser	Ile	Ala	Asp	Leu	His
180								185				190			
Thr	Lys	Gly	Ile	Lys	Val	Gly	Cys	Trp	Thr	Ile	Arg	Asp	Glu	Asn	Ala
195								200				205			
Phe	Gly	Ile	Ala	Gln	Gln	Ala	Gly	Val	Asp	Tyr	Ala	Thr	Val	Ser	Asp
210								215				220			
Pro	Ser	Arg	Phe	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Glu	Leu	His	Trp	
225								230				235			

```
<210> 205
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1291)
<223> RXA01436
```

<400> 205.																
gcctaaacaa	accagtc	aac	gacctttccc	gtggcgcaac	agtccctgac	atcg	tcaaca	60								
cagtagccat	cacagcaatt	caggcaggag	gacgcagcta	atg	gca	ttg	gca	ctt	115							
					Met	Ala	Leu	Ala	Leu							
					1				5							
ggt	ttg	aac	tcc	ggt	tca	tct	tcc	atc	aaa	ttc	cag	ctg	gtc	aac	ccc	163
Val	Leu	Asn	Ser	Gly	Ser	Ser	Ser	Ile	Lys	Phe	Gln	Leu	Val	Asn	Pro	
				10					15						20	
gaa	aac	tct	gcc	atc	gac	gag	cca	tat	ggt	tct	ggt	ctt	gtg	gag	cag	211
Glu	Asn	Ser	Ala	Ile	Asp	Glu	Pro	Tyr	Val	Ser	Gly	Leu	Val	Glu	Gln	
			25					30					35			
att	ggt	gag	cca	aac	ggc	cgc	atc	gta	ctc	aaa	ata	gag	ggt	gaa	aaa	259
Ile	Gly	Glu	Pro	Asn	Gly	Arg	Ile	Val	Leu	Lys	Ile	Glu	Gly	Glu	Lys	
		40					45					50				
tat	acc	cta	gag	aca	ccc	atc	gca	gat	cac	tcc	gaa	ggc	cta	aac	ctg	307
Tyr	Thr	Leu	Glu	Thr	Pro	Ile	Ala	Asp	His	Ser	Glu	Gly	Leu	Asn	Leu	
	55					60					65					
gcg	ttc	gat	ctc	atg	gac	cag	cac	aac	tgt	ggt	cct	tcc	caa	ctg	gaa	355
Ala	Phe	Asp	Leu	Met	Asp	Gln	His	Asn	Cys	Gly	Pro	Ser	Gln	Leu	Glu	
70					75					80					85	
atc	acc	gca	ggt	gga	cac	cgc	gtg	gtc	cac	ggc	gga	atc	ttg	ttc	tcc	403
Ile	Thr	Ala	Val	Gly	His	Arg	Val	Val	His	Gly	Gly	Ile	Leu	Phe	Ser	
				90					95					100		
gca	ccg	gaa	ctt	atc	act	gat	gaa	atc	gtg	gaa	atg	atc	cgc	gat	ctc	451
Ala	Pro	Glu	Leu	Ile	Thr	Asp	Glu	Ile	Val	Glu	Met	Ile	Arg	Asp	Leu	
			105					110					115			
att	cca	ctc	gca	cca	ctg	cac	aac	cct	gca	aac	gtt	gac	ggc	att	gat	499

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp	
		120					125					130				
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp	
		135				140					145					
acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile	
		150			155					160					165	
aac	aag	gat	gtc	gca	gct	gaa	cac	gga	atc	agg	cgc	tat	ggg	ttc	cac	643
Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His	
				170					175					180		
ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu	
			185					190					195			
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly	
		200					205					210				
gca	tcc	atg	gct	gct	gtt	caa	ggg	ggc	cgt	gcg	gta	gat	act	tcc	atg	787
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met	
		215				220					225					
ggg	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggg	acc	cga	agc	ggg	gac	835
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp	
					235					240					245	
att	gat	cca	ggg	atc	gtc	ttc	cac	ctt	tcc	cgc	acc	gct	ggc	atg	agc	883
Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser	
				250					255					260		
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tgc	ggg	gta	aag	gga	931
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly	
			265					270					275			
ctt	tcc	ggg	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn	
		280					285					290				
aat	gat	caa	gat	gcc	tgg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu	
		295				300					305					
cgc	cgc	tac	ctc	ggg	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr	
					315					320					325	
atc	gtg	ttc	acc	gcc	ggg	gtc	ggg	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu	
				330					335					340		
gat	gcc	ttg	gca	ggg	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu	
			345					350					355			
cgt	aac	gca	ttg	cca	aac	gat	ggg	cct	cga	ttg	att	tcc	acc	gat	gcc	1219
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala	

360 365 370
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385

gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

<210> 206

<211> 397

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
 1 5 10 15

Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
 20 25 30

Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45

Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60

Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65 70 75 80

Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
 85 90 95

Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
 100 105 110

Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
 115 120 125

Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
 130 135 140

Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
 145 150 155 160

Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
 165 170 175

Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
 180 185 190

Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
 195 200 205

His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
 210 215 220

Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
 225 230 235 240

```
<210> 207
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(904)  
<223> RXA00686
```

ataggcttga	acaatacgtc	gttacactgg	ccgatttgat	acctttcaaa	acttttaccc	60
ttcatcgag	tgccagggga	acttagagga	gcattaaata	atg	gcg gga gga aat	115
				Met	Ala Gly Gly Asn	
				1		5
cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga	163					
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly						
10 15 20						
gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag	211					
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu						
25 30 35						
ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta	259					
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu						
40 45 50						

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
 150 155 160 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
 250 255 260

gca gaa cga aaa ggc gat acc taaaccgcgc ctccatctgc ata 927
 Ala Glu Arg Lys Gly Asp Thr
 265

<210> 208

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
 1 5 10 15

Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
 20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
 35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
 50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
 65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
 145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
 245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
 260 265

<210> 209

<211> 1158

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1135)

<223> RXA00246

<400> 209

ttgcaaggat tgtaatttaa ggcacatcta tgtcgggtgtg aaattacatg tgccagaaga 60

gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115
 Met Thr Thr Ala Ala
 1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
 Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
 10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
 Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
 25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
 Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
 40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
 Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
 55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
 Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
 70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
 Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
 90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
 Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
 105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
 Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
 120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
 Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
 135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
 Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
 150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
 Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
 170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
 Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met
 185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739
 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
 200 205 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787
 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
 215 220 225

gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
 230 235 240 245

act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
 250 255 260

cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
 265 270 275

gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
 280 285 290

ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
 295 300 305

cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
 310 315 320 325

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
 330 335 340

gcg att cgt ttc taacggattg tgttgaaact gct 1158
 Ala Ile Arg Phe
 345

<210> 210

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
 1 5 10 15

Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
 20 25 30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
 65 70 75 80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
 85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
 245 250 255
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
 260 265 270
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
 275 280 285
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
 290 295 300
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
 305 310 315 320
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
 325 330 335
 Ile Asp Gly Arg Val Ala Ile Arg Phe
 340 345

<210> 211

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01571

<400> 211

aaactacctg	ctgagagctt	tgtaatttac	ggtgtggttg	tgagagggtg	cgctcgagaag	60
cgctcgtagg	cgcttttgat	ttttcggtag	gctaactggg	gtg agt atc tca gta	115	
				Val Ser Ile Ser Val	5	
				1		
aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc	163					
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile	20					
	10		15			
att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa	211					
Ile Glu Arg Arg Asp Pro Arg Ala Asp Val Val Ile Asp Ile Lys	35					
	25		30			
gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg	259					
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp	50					
	40		45			
ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt	307					
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val	65					
	55		60			
gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc	355					
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg	85					
	70		75			
gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc	403					
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys	100					
	90		95			
gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac	451					
Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr	115					
	105		110			
aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa	499					
Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu	130					
	120		125			
aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt	547					
Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu	145					
	135		140			
aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac	595					
Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr	165					
	150		155			
tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc	643					
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val	180					
	170		175			
atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc	691					
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser	195					
	185		190			
caa ggg tgc tgaggttacc gttctgtccc gtt	723					
Gln Gly Cys	200					

<210> 212

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 213

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA01572

<400> 213

ctgctgtgcg caggcacac cacctactcc ccaatcgctc gctggaacgt taaagaaggc 60

gacaaagtag cagtcacggg cctcggcggg actcggacac atg ggt gtc cag atc 115
 Met Gly Val Gln Ile
 1 5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
 10 15 20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160

taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
 1 5 10 15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160
 Val Glu Ala Val

<210> 215
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXA01758

<400> 215
 ccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60
 gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
 55 60 65
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
 70 75 80 85
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

90	95	100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser 105 110 115			451
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu 120 125 130			499
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly 135 140 145			547
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp 150 155 160 165			595
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu 170 175 180			643
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala 185 190 195			691
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His 200 205 210			739
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu 215 220 225			787
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu 230 235 240 245			835
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile 250 255 260			883
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met 265 270 275			931
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr 280 285 290			979
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile 295 300 305			1027
gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser 310 315 320 325			1075
gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser 330 335			1117

taatgccaac agcaagccca att

1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met	Pro	Lys	Tyr	Ile	Ala	Met	Gln	Val	Ser	Glu	Ser	Gly	Ala	Pro	Leu
1				5					10					15	

Ala	Ala	Asn	Leu	Val	Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg
		20						25					30		

Val	Glu	Ile	Ala	Ala	Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala
		35					40					45			

Ala	Ala	Ser	Gly	Lys	His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu
		50				55					60				

Ile	Ala	Gly	Thr	Ile	Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr
65					70					75					80

Val	Gly	Asp	Arg	Val	Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp
				85					90					95	

Cys	Ala	Phe	Cys	Arg	Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys
			100					105					110		

Ile	Pro	Gly	Val	Ser	Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val
		115					120					125			

Pro	Ala	Glu	Ala	Leu	Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu
		130				135					140				

Pro	Ala	Pro	Met	Gly	Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg
145					150					155					160

Asn	Leu	Lys	Leu	Asp	Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly
				165					170					175	

Gly	Leu	Val	Arg	Leu	Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg
		180					185						190		

Thr	Ile	Thr	Ile	Ala	Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln
		195					200					205			

Leu	Gly	Ala	Asn	His	Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln
	210					215					220				

Ala	Leu	Phe	Glu	Leu	Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser
225					230					235					240

Thr	Thr	Glu	Pro	Leu	Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly
				245					250					255	

Gln	Leu	Thr	Ile	Ile	Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala
			260					265					270		

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 217
 <211> 1641
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1618)
 <223> RXA02539

<400> 217
 ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcggt gaccaagtgt cacctgacgc 60
 acaggtagtgt ctcaggtgga ggtggcccaa aggagaccca atg act gtc tac gca 115
 Met Thr Val Tyr Ala
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
 105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile	
120 125 130	
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala	
135 140 145	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
150 155 160 165	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
170 175 180	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser	
185 190 195	
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val	
200 205 210	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser	
215 220 225	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc	835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
230 235 240 245	
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
 360 365 370
 aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt 1267
 Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
 375 380 385
 ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga 1315
 Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
 390 395 400 405
 cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt 1363
 Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
 410 415 420
 att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt 1411
 Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
 425 430 435
 gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga 1459
 Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
 440 445 450
 gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt 1507
 Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
 455 460 465
 gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg 1555
 Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
 470 475 480 485
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500
 cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 218

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
 1 5 10 15
 Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
 20 25 30
 Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45
 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60
 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

311

405	410	415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala		
420	425	430
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala		
435	440	445
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala		
450	455	460
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn		
465	470	475
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val		
485	490	495
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe		
500	505	

<210> 219
 <211> 430
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(430)
 <223> RXN03061

<400> 219
 ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60
 gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc 115
 Val Ser Leu Thr Phe
 1 5
 cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
 Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
 10 15 20
 cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
 His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
 25 30 35
 ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
 Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
 40 45 50
 acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
 Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
 55 60 65
 atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
 Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
 70 75 80 85
 gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
 Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
 90 95 100

40	45	50	
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc			307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser			
55	60	65	
tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc			355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly			
70	75	80	85
agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg			403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val			
90	95	100	
ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc			451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe			
105	110	115	
gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc			499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile			
120	125	130	
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg			547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Thr Val Trp Thr			
135	140	145	
agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga			595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly			
150	155	160	165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga			643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly			
170	175	180	
ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt			691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu			
185	190	195	
gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata			744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu			
200	205		
tat			747

<210> 222

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Val	Glu	Ala	Gln	Phe	Thr	Ser	Pro	Leu	Leu	Asn	Asn	Gly	Gln	Thr	Cys
1				5					10					15	

Phe	Leu	Gly	Thr	Arg	Ile	Leu	Ala	Pro	Lys	Ser	Arg	Tyr	Ala	Glu	Val
			20					25					30		

Val	Asp	Ala	Phe	Thr	Ala	Phe	Ala	Gly	Ser	Leu	Gln	Val	Gly	Val	Thr
	35						40					45			

Ser	Ser	Pro	Asp	Thr	Gln	Ile	Gly	Pro	Met	Ala	Thr	Ala	Arg	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg		
65	70	75
Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe		
	85	90
Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala		
	100	105
Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp		
	115	120
Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly		
	130	135
Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg		
	145	150
Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro		
	165	170
Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu		
	180	185
Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu		
	195	200

<210> 223

<211> 881

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(858)

<223> RXN01340

<400> 223

aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg	48
Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro	
1	5
cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg	96
Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser	
	20
gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga	144
Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly	
	35
tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg	192
Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu	
	50
ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac	240

Leu	Arg	Thr	Ser	Met	Glu	Leu	Gly	Gly	Asn	Ala	Ala	Phe	Val	Ile	Asp	
65					70				75						80	
gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa 288																
Glu	Ala	Ala	Asp	Leu	Asp	Glu	Ala	Val	Ser	Gly	Ala	Ile	Ala	Ala	Lys	
				85					90					95		
ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt 336																
Leu	Arg	Asn	Ala	Gly	Gln	Val	Cys	Ile	Ala	Ala	Asn	Arg	Phe	Leu	Val	
			100					105					110			
cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg 384																
His	Glu	Ser	Arg	Ala	Ala	Glu	Phe	Thr	Ser	Lys	Leu	Ala	Thr	Ala	Met	
		115					120					125				
cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg 432																
Gln	Asn	Thr	Pro	Ile	Gly	Pro	Val	Ile	Ser	Ala	Arg	Gln	Arg	Asp	Arg	
		130				135					140					
atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc 480																
Ile	Ala	Ala	Leu	Val	Asp	Glu	Ala	Ile	Thr	Asp	Gly	Ala	Arg	Leu	Ile	
145					150					155				160		
atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc 528																
Ile	Gly	Gly	Glu	Val	Pro	Asp	Gly	Ser	Gly	Phe	Phe	Tyr	Pro	Ala	Thr	
			165					170						175		
atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc 576																
Ile	Leu	Ala	Asp	Val	Pro	Ala	Gln	Ser	Arg	Ile	Val	His	Glu	Glu	Ile	
			180					185					190			
ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624																
Phe	Gly	Pro	Val	Ala	Thr	Ile	Ala	Thr	Phe	Thr	Asp	Leu	Ala	Glu	Gly	
		195					200					205				
gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672																
Val	Ala	Gln	Ala	Asn	Ser	Thr	Glu	Phe	Gly	Leu	Ala	Ala	Tyr	Gly	Phe	
	210					215					220					
agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720																
Ser	Asn	Asn	Val	Lys	Ala	Thr	Gln	Tyr	Met	Ala	Glu	His	Leu	Glu	Ala	
225					230					235				240		
gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768																
Gly	Met	Val	Gly	Ile	Asn	Arg	Gly	Ala	Ile	Ser	Asp	Pro	Ala	Ala	Pro	
				245					250					255		
ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816																
Phe	Gly	Gly	Ile	Gly	Gln	Ser	Gly	Phe	Gly	Arg	Glu	Gly	Gly	Thr	Glu	
			260					265					270			
gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858																
Gly	Ile	Glu	Glu	Tyr	Leu	Ser	Val	Arg	Tyr	Leu	Ala	Leu	Pro			
		275					280					285				
tgacacatga gctgtccggt gaa 881																

<210> 224

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175

Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190

Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255

Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270

Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285

<210> 225

<211> 1686

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

```

cagtggacaa ctacttggcg ggtctttaa atg cagctgtgaa ggattctgca taagctgggc 60
accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt 115
                                         Met Ile Lys Arg Leu
                                         1           5

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg 163
Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu
                        10                        15                        20

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt 211
Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe
                        25                        30                        35

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc 259
Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val
                        40                        45                        50

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac 307
Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His
                        55                        60                        65

acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg 355
Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu
                        70                        75                        80                        85

gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca 403
Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr
                        90                        95                        100

ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc 451
Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile
                        105                        110                        115

acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag 499
Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys
                        120                        125                        130

aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat 547
Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr
                        135                        140                        145

gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta 595
Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu
                        150                        155                        160                        165

act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca 643
Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala
                        170                        175                        180

gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg 691
Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met
                        185                        190                        195

```

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
 440 445 450
 gtg tcc acg cct ctg ggt ggc atg aag cag tcc ggg ctg ggg cac cgc 1507
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
 455 460 465
 cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
 470 475 480 485
 gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
 490 495 500
 gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
 505 510 515
 aaa gtt ttg ccg tagcaaaaag ccggaccctt gct 1686
 Lys Val Leu Pro
 520

<210> 226

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
 1 5 10 15
 Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
 20 25 30
 Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45
 Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60
 Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80
 Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95
 Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110
 Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125
 Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140
 Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
 290 295 300
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
 305 310 315 320
 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
 325 330 335
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
 340 345 350
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
 355 360 365
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
 370 375 380
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
 385 390 395 400
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
 435 440 445
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
 450 455 460
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
 465 470 475 480
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

aat act ccg ggc aaa gaa aac cgt gtg tac cgc gta gcc aag ggc gtt 547
Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val
135 140 145

gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc	595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg	
150 155 160 165	
tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct	643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro	
170 175 180	
gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt	691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe	
185 190 195	
gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca	739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala	
200 205 210	
gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg	787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu	
215 220 225	
att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg	835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu	
230 235 240 245	
gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc	883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly	
250 255 260	
aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	

cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag 1315
 Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
 390 395 400 405

ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag 1363
 Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys
 410 415 420

gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg 1411
 Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met
 425 430 435

gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc 1459
 Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
 440 445 450

ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg 1507
 Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
 455 460 465

atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552
 Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser
 470 475 480

taattgtttt tcgacgtaac ccc 1575

<210> 228

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Val Thr Ala Thr Phe Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly
 1 5 10 15

Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
 20 25 30

Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
 35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
 50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
 65 70 75 80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
 85 90 95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
 100 105 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
 115 120 125

Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
 130 135 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu

145	150	155	160
Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala	165	170	175
Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile	180	185	190
Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser	195	200	205
Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His	210	215	220
Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg	225	230	235
Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala	245	250	255
Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp	260	265	270
Ile Asp Ala Ala Ala Gln Ala Ala Val Gly Ala Phe Leu His Gln	275	280	285
Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val	290	295	300
His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro	305	310	315
Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn	325	330	335
Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys	340	345	350
Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val	355	360	365
His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg	370	375	380
Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu	385	390	395
Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala	405	410	415
Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln	420	425	430
Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu	435	440	445
Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe	450	455	460
Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly	465	470	475
			480

cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc	643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro	
170 175 180	
gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct	691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala	
185 190 195	
gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac	739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His	
200 205 210	
att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa	787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu	
215 220 225	
gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg	835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
230 235 240 245	
ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act	883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr	
250 255 260	
ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg	931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp	
265 270 275	
gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct	979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala	
280 285 290	
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act	1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr	
295 300 305	
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct	1075
Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro	
310 315 320 325	
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag	1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
330 335 340	
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg	1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
345 350 355	
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg	1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala	
360 365 370	
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag	1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys	
375 380 385	
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc	1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile	
390 395 400 405	

ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala 410 415 420	1363
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp 425 430 435	1411
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu 440 445 450	1459
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp 455 460 465	1507
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu 470 475 480 485	1555
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val 490 495 500	1603
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu 505 510 515	1651
act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala 520 525 530	1699
gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala 535 540 545	1747
atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser 550 555 560 565	1795
gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala 570 575 580	1843
tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr 585 590 595	1891
gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser 600 605 610	1939
act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln 615 620 625	1987
gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa Ala Leu Gln Arg Pro Leu Leu Gly 630 635	2034

<210> 230
 <211> 637
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230

Met Ala Glu Thr Lys Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe
 1 5 10 15
 Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile
 20 25 30
 Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
 35 40 45
 Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
 50 55 60
 Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
 65 70 75 80
 Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
 85 90 95
 Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
 100 105 110
 Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
 115 120 125
 Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
 130 135 140
 Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
 145 150 155 160
 Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
 165 170 175
 Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
 180 185 190
 Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
 195 200 205
 Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
 210 215 220
 Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
 225 230 235 240
 Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
 245 250 255
 Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
 260 265 270
 Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
 275 280 285
 Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile

290					295					300				
Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr	305				310					315				320
Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser				325					330				335	
Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala			340					345				350		
Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val		355					360					365		
Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp	370					375				380				
Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly	385					390				395				400
Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp				405				410					415	
Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu			420					425					430	
Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser		435					440				445			
Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu	450				455					460				
Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly	465				470				475					480
Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly			485					490					495	
Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile		500						505					510	
Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr		515					520				525			
Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu	530					535				540				
Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile	545				550				555					560
Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met			565					570					575	
Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser			580				585						590	
Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro		595				600					605			
Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp	610					615				620				

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
625 630 635

<210> 231
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1119)
<223> RXN01143

<400> 231
atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct 48
Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
1 5 10 15
cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96
His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
20 25 30
gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144
Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
35 40 45
ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
50 55 60
aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag 240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
65 70 75 80
cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
85 90 95
ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
100 105 110
gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
115 120 125
tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
130 135 140
acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
145 150 155 160
ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
165 170 175
cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt 576

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val	
180 185 190	
cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg	624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp	
195 200 205	
gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc	672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr	
210 215 220	
acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac	720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn	
225 230 235 240	
gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa	768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu	
245 250 255	
gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc	816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro	
260 265 270	
gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc	864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val	
275 280 285	
acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc	912
Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile	
290 295 300	
aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag	960
Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln	
305 310 315 320	
gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac	1008
Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr	
325 330 335	
gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa	1056
Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu	
340 345 350	
gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt	1104
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val	
355 360 365	
gaa tcg acc gag gca taaggagaga cccaagatgg cta	1142
Glu Ser Thr Glu Ala	
370	

<210> 232

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
1 5 10 15

His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

340 345 350
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
 355 360 365
 Glu Ser Thr Glu Ala
 370
 <210> 233
 <211> 793
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(793)
 <223> RXN01146
 <400> 233
 tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccactcccgc 60
 cacggttgca agccgtggtc gatccgccgc cctgagcgg atg aca ggt gca aag 115
 Met Thr Gly Ala Lys
 1 5
 gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
 Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
 10 15 20
 att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
 Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
 25 30 35
 aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
 Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
 40 45 50
 gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
 Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
 55 60 65
 gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
 Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
 70 75 80 85
 gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
 Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
 90 95 100
 agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
 Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
 105 110 115
 atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac 499
 Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
 120 125 130
 gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
 Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
 135 140 145

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165

gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180

cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
 185 190 195

atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
 200 205 210

aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
 215 220 225

atc cca 793
 Ile Pro
 230

<210> 234

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala
 1 5 10 15

Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp
 20 25 30

Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
 35 40 45

Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80

Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95

Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110

Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
 115 120 125

Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
 130 135 140

Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
 145 150 155 160

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
 165 170 175

Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
 180 185 190

Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
 195 200 205

Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
 210 215 220

Ala Glu Tyr Thr Gly Ile Pro
 225 230

<210> 235

<211> 639

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(616)

<223> RXN01144

<400> 235

ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60

gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tct gac 115
 Met Ala Asn Ser Asp
 1 5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
 10 15 20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
 25 30 35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
 Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
 40 45 50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
 55 60 65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
 70 75 80 85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
 90 95 100

acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
 Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
 105 110 115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
 Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
 120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
 Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
 135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
 Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
 150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
 Thr Met Ala Pro Ala Lys Ile
 170

<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
 1 5 10 15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
 165 170

<210> 237

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

tgctggtcta ttgtggcgac cgagggcctt tgaagggtcg acaaactgta taaggccttg 60

aatcttgaga atttattttg aggaagcaag aggaagtgtc	atg agc aaa gtt gca	115
	Met Ser Lys Val Ala	
	1 5	

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag	163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys	
10 15 20	

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag	211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln	
25 30 35	

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa	259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln	
40 45 50	

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac	307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp	
55 60 65	

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta	355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu	
70 75 80 85	

gta aac aac gcc ggc ggc atc gca caa att aag cca ctt ctg gaa gtc acc	403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr	
90 95 100	

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt	451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe	
105 110 115	

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa	499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys	
120 125 130	

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca	547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro	
135 140 145	

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc	595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr	
150 155 160 165	

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc	643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala	
170 175 180	

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc	691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala	
185 190 195	

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
 200 205 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
 215 220 225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc 835
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
 230 235 240 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc 884
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
 250 255

tttcccgcac tca 897

<210> 238

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
 1 5 10 15

Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60

Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80

Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95

Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110

Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125

Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140

Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160

Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175

His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 239
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXA02453

<400> 239
 aaccaacaaa ggatcatctca accggccttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
 Met Lys Ser Ile Phe
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
 Leu Gln Asp Ala Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 240
 <211> 251
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 240
 Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
 1 5 10 15
 Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30
 Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45
 Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60
 Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80
 Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 241
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXS01758

<400> 241
 ccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60
 gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027

Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335

taatgccaac agcaagccca att 1140

<210> 242

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
 1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
 260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 243
 <211> 1665
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1642)
 <223> RXA02737

<400> 243
 agcacgctgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccggt 60

acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
 Val Ser Thr Asn Thr
 1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
 10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
 Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
 25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
 Gly Asp Leu Ala Arg Lys Lys Leu Pro Ala Ile Tyr Asp Leu Ala
 40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
 Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
 55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

70	75	80	85	
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc				403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu				
90		95	100	
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct				451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala				
105		110	115	
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc				499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly				
120		125	130	
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc				547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe				
135		140	145	
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc				595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr				
150		155	160	165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac				643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn				
170		175	180	
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca				691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro				
185		190	195	
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt				739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val				
200		205	210	
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg				787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu				
215		220	225	
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat				835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp				
230		235	240	245
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc				883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala				
250		255	260	
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc				931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala				
265		270	275	
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag				979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys				
280		285	290	
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc				1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr				
295		300	305	
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc				1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val				
310		315	320	325

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag 1123
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu
330 335 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt 1171
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
440 445 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
455 460 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
505 510

gcaaaaaatg atc 1665

<210> 244

<211> 514

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp
1 5 10 15

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val
 20 25 30
 Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
 50 55 60
 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
 290 295 300
 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320
 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

[illegible]

```
<210> 245
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1180)
<223> RXA02738
```

```

<400> 245
ttgtttgtaa tcggtacaaa gggctcttaag cacatccctt acttgcctgc tctccttgag 60
cacagttcaa gaacaattct tttaaggaaa atttagtttc atg tot cac att gat 115
                                         Met Ser His Ile Asp
                                         1                               5

gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
                        10                        15                        20

gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
                        25                        30                        35

```


gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc	259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser	
40 45 50	
aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc	307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
55 60 65	
gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc	355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
70 75 80 85	
aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac	403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
90 95 100	
gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc	451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
105 110 115	
gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt	499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
120 125 130	
cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca	547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc	595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
150 155 160 165	
ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc	643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct	691
Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
185 190 195	
gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc	739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
200 205 210	
ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca	787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala	
215 220 225	
ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc	835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe	
230 235 240 245	
gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg	883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
250 255 260	
gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt	931
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc	979

Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
 280 285 290
 atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305
 aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
 310 315 320 325
 ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340
 gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala
 345 350 355
 cgc ctg aag tagaatcagc acgctgcatc agt 1203
 Arg Leu Lys
 360
 <210> 246
 <211> 360
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 246
 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
 1 5 10 15
 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
 20 25 30
 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
 35 40 45
 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60
 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80
 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95
 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 100 105 110
 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125
 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
 130 135 140
 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 145 150 155 160
 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala

165						170						175					
Ala	Phe	Ile	Glu	Gly	Ile	Lys	Gln	Ala	Ala	Ala	Asn	Gly	His	Asp	Val		
180						185						190					
Ser	Lys	Ile	His	Ser	Val	Ala	Ser	Phe	Phe	Val	Ser	Arg	Val	Asp	Val		
195						200						205					
Glu	Ile	Asp	Lys	Arg	Leu	Glu	Ala	Ile	Gly	Ser	Asp	Glu	Ala	Leu	Ala		
210						215						220					
Leu	Arg	Gly	Lys	Ala	Gly	Val	Ala	Asn	Ala	Gln	Arg	Ala	Tyr	Ala	Val		
225						230						235					
Tyr	Lys	Glu	Leu	Phe	Asp	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Thr		
245						250						255					
Gln	Arg	Pro	Leu	Trp	Ala	Ser	Thr	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala		
260						265						270					
Ala	Thr	Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr		
275						280						285					
Met	Pro	Glu	Gly	Thr	Ile	Asp	Ala	Val	Leu	Glu	Gln	Gly	Asn	Leu	His		
290						295						300					
Gly	Asp	Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser		
305						310						315					
Gln	Leu	Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu		
325						330						335					
Glu	Thr	Glu	Gly	Val	Asp	Lys	Phe	Val	Ala	Ser	Trp	Ser	Glu	Leu	Leu		
340						345						350					
Glu	Ser	Met	Glu	Ala	Arg	Leu	Lys										
355						360											

<210> 247

<211> 2223

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2200)

<223> RXA02739

<400> 247

cctttgccaa atttgaacca attaacctaa gtcgtagatc tgatcatcgg atctaacgaa 60

aacgaaccaa	aactttggtc	ccggtttaac	ccaggaagga	ttg	acc	acc	ttg	acg	115
				Leu	Thr	Thr	Leu	Thr	
				1				5	

ctg	tca	cct	gaa	ctt	cag	gcg	ctc	act	gta	cgc	aat	tac	ccc	tct	gat	163
Leu	Ser	Pro	Glu	Leu	Gln	Ala	Leu	Thr	Val	Arg	Asn	Tyr	Pro	Ser	Asp	
				10				15						20		

tgg	tcc	gat	gtg	gac	acc	aag	gct	gta	gac	act	gtt	cgt	gtc	ctc	gct	211
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala	
			25					30					35			
gca	gac	gct	gta	gaa	aac	tgt	ggc	tcc	ggc	cac	cca	ggc	acc	gca	atg	259
Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met	
			40				45					50				
agc	ctg	gct	ccc	ctt	gca	tac	acc	ttg	tac	cag	cgg	gtt	atg	aac	gta	307
Ser	Leu	Ala	Pro	Leu	Ala	Tyr	Thr	Leu	Tyr	Gln	Arg	Val	Met	Asn	Val	
	55					60				65						
gat	cca	cag	gac	acc	aac	tgg	gca	ggc	cgt	gac	cgc	ttc	gtt	ctt	tct	355
Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser	
	70				75				80						85	
tgt	ggc	cac	tcc	tct	ttg	acc	cag	tac	atc	cag	ctt	tac	ttg	ggt	gga	403
Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly	
			90				95						100			
ttc	ggc	ctt	gag	atg	gat	gac	ctg	aag	gct	ctg	cgc	acc	tgg	gat	tcc	451
Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser	
			105				110					115				
ttg	acc	cca	gga	cac	cct	gag	tac	cgc	cac	acc	aag	ggc	gtt	gag	atc	499
Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile	
		120				125					130					
acc	act	ggc	cct	ctt	ggc	cag	ggt	ctt	gca	tct	gca	gtt	ggt	atg	gcc	547
Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala	
	135				140				145							
atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu	
	150				155				160						165	
ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggt	643
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly	
			170				175						180			
gac	ctg	cag	gaa	ggt	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr	
		185					190					195				
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser	
		200				205						210				
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg	
	215				220					225						
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp	
	230			235				240					245			
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys	
			250				255					260				
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro	

265	270	275	
act atg atg aac acc ggt gct gtg cac ggt gct gct ctt ggc gca gct			979
Thr Met Met Asn Thr Gly Ala Val His Gly Ala Ala Leu Gly Ala Ala			
280	285	290	
gag gtt gca gca acc aag act gag ctt gga ttc gat cct gag gct cac			1027
Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe Asp Pro Glu Ala His			
295	300	305	
ttc gcg atc gac gat gag gtt atc gct cac acc cgc tcc ctc gca gag			1075
Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr Arg Ser Leu Ala Glu			
310	315	320	325
cgc gct gca cag aag aag gct gca tgg cag gtc aag ttc gat gag tgg			1123
Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val Lys Phe Asp Glu Trp			
330	335	340	
gca gct gcc aac cct gag aac aag gct ctg ttc gat cgc ctg aac tcc			1171
Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe Asp Arg Leu Asn Ser			
345	350	355	
cgt gag ctt cca gcg ggc tac gct gac gag ctc cca aca tgg gat gca			1219
Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu Pro Thr Trp Asp Ala			
360	365	370	
gat gag aag ggc gtc gca act cgt aag gct tcc gag gct gca ctt cag			1267
Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser Glu Ala Ala Leu Gln			
375	380	385	
gca ctg ggc aag acc ctt cct gag ctg tgg ggc ggt tcc gct gac ctc			1315
Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu			
390	395	400	405
gca ggt tcc aac aac acc gtg atc aag ggc tcc cct tcc ttc ggc cct			1363
Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser Pro Ser Phe Gly Pro			
410	415	420	
gag tcc atc tcc acc gag acc tgg tct gct gag cct tac ggc cgt aac			1411
Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu Pro Tyr Gly Arg Asn			
425	430	435	
ctg cac ttc ggt atc cgt gag cac gct atg gga tcc atc ctc aac ggc			1459
Leu His Phe Gly Ile Arg Glu His Ala Met Gly Ser Ile Leu Asn Gly			
440	445	450	
att tcc ctc cac ggt ggc acc cgc cca tac ggc gga acc ttc ctc atc			1507
Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly Gly Thr Phe Leu Ile			
455	460	465	
ttc tcc gac tac atg cgt cct gca gtt cgt ctt gca gct ctc atg gag			1555
Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu Ala Ala Leu Met Glu			
470	475	480	485
acc gac gct tac tac gtc tgg acc cac gac tcc atc ggt ctg ggc gaa			1603
Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser Ile Gly Leu Gly Glu			
490	495	500	
gat ggc cca acc cac cag cct gtt gaa acc ttg gct gca ctg cgc gcc			1651
Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu Ala Ala Leu Arg Ala			
505	510	515	

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
 600 605 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca 1987
 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
 615 620 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223
 Ala Lys Asp Ser Ile Asn Gly
 695 700

<210> 248

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg
 1 5 10 15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
 35 40 45
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
 50 55 60
 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
 195 200 205
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
 355 360 365
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
 500 505 510
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
 660 665 670
 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

675	680	685	
Ala Val Val Ala Ala Ala	Lys Asp Ser Ile Asn Gly		
690	695	700	
<p><210> 249 <211> 793 <212> DNA <213> Corynebacterium glutamicum</p> <p><220> <221> CDS <222> (48)..(770) <223> RXA00965</p> <p><400> 249 agattgcggg cctcggcttc attgaaaaca agacgggtgtt tgaataaatg aca act 56 <div style="text-align: right;">Met Thr Thr 1</div></p> <p>ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc 104 Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly <div style="display: flex; justify-content: space-around;"><div>5</div><div>10</div><div>15</div></div></p> <p>aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc 152 Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe <div style="display: flex; justify-content: space-around;"><div>20</div><div>25</div><div>30</div><div>35</div></div></p> <p>ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala <div style="display: flex; justify-content: space-around;"><div>40</div><div>45</div><div>50</div></div></p> <p>cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala <div style="display: flex; justify-content: space-around;"><div>55</div><div>60</div><div>65</div></div></p> <p>aat act ggt gag gaa acc cca atg tac gtg tcg cca gaa gcg cgc aac 296 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn <div style="display: flex; justify-content: space-around;"><div>70</div><div>75</div><div>80</div></div></p> <p>gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn <div style="display: flex; justify-content: space-around;"><div>85</div><div>90</div><div>95</div></div></p> <p>ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr <div style="display: flex; justify-content: space-around;"><div>100</div><div>105</div><div>110</div><div>115</div></div></p> <p>tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr <div style="display: flex; justify-content: space-around;"><div>120</div><div>125</div><div>130</div></div></p> <p>gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile <div style="display: flex; justify-content: space-around;"><div>135</div><div>140</div><div>145</div></div></p> <p>cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu <div style="display: flex; justify-content: space-around;"><div>150</div><div>155</div><div>160</div></div></p>			

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175

caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195

cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210

ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225

act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
 230 235 240

tagtttccac acattcttaa atg 793

<210> 250

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala
 1 5 10 15

Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
 20 25 30

Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45

Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60

His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80

Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95

Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110

Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125

Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140

Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160

Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
 210 215 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
 225 230 235 240

Leu

<210> 251
 <211> 1575
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1552)
 <223> RXN00999

<400> 251
 cctcctgtga cctggtaaaa tcgccactac ccccaaattg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc	499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser	
120 125 130	
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
 360 365 370

 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
 470 475 480

 taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15

 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
 465 470 475 480

Glu Val Glu Ala

<210> 253
 <211> 1537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1537)
 <223> FRXA00999

<400> 253
 cctcctgtga cctggtaaaa tcgccactac ccccaaattg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
 120 125 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc	1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys	
360 365 370	

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc 1537
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 470 475

<210> 254

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15

 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 465 470 475

<210> 255
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02596

<400> 255
 aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60
 gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35
 cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50
 acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65
 aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85
 tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100
 ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115
 cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130
 tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145
 cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
ggt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac	979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His	
280 285 290	
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat	1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp	
295 300 305	
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat	1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp	
310 315 320 325	
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag	1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys	
330 335 340	
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg	1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu	
345 350 355	
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct	1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala	
360 365 370	
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt	1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe	
375 380 385	
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag	1313
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His	
390 395 400	
ggcatctccc aca	1326

<210> 256
 <211> 401
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256

```

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
  1           5           10           15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
          20           25           30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
      35           40           45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
      50           55           60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
      65           70           75           80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
          85           90           95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
      100           105           110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
      115           120           125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
      130           135           140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
      145           150           155           160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
          165           170           175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
      180           185           190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
      195           200           205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
      210           215           220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
      225           230           235           240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
          245           250           255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
          260           265           270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
      275           280           285

```

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
 385 390 395 400

His

<210> 257

<211> 512

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(489)

<223> FRXA02596

<400> 257

cct gtc gtc tac acc ggc cca ctc gac ctc tac ttc aac tac gca gag	48
Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu	
1 5 10 15	
ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa	96
Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu	
20 25 30	
acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac	144
Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp	
35 40 45	
gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt	192
Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg	
50 55 60	
gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc	240
Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser	
65 70 75 80	
cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca	288
Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro	
85 90 95	

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 cgc gga cac taaaaggaag ggcattctccc aca 512
 Arg Gly His

<210> 258
 <211> 163
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15

 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 Arg Gly His

<210> 259
 <211> 598
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> FRXA02642

<400> 259

aaggatatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60

gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag 598
 Gln

<210> 260
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 260
 Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
 1 5 10 15
 Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30
 Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln
 165

<210> 261
 <211> 668
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(645)
 <223> RXA02572

<400> 261
 gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48
 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15
 gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

Ala	Gly	Leu	Gly	Phe	Gly	Gly	Gly	Cys	Leu	Pro	Lys	Asp	Ile	Arg	Ala	
	35						40					45				
ttc	atg	gca	cgc	gcg	ggc	gaa	ttg	ggg	gct	gac	cag	gca	tta	acg	ttc	192
Phe	Met	Ala	Arg	Ala	Gly	Glu	Leu	Gly	Ala	Asp	Gln	Ala	Leu	Thr	Phe	
	50					55					60					
ttg	cgt	gag	gtc	gat	tcc	atc	aat	atg	cgt	cgt	cgc	gac	cgt	gtg	gtg	240
Leu	Arg	Glu	Val	Asp	Ser	Ile	Asn	Met	Arg	Arg	Arg	Asp	Arg	Val	Val	
	65				70				75					80		
cag	ctg	gcc	aaa	gag	atg	tgt	ggc	ggg	tcg	ctg	ctg	ggc	aag	cgg	gtt	288
Gln	Leu	Ala	Lys	Glu	Met	Cys	Gly	Gly	Ser	Leu	Leu	Gly	Lys	Arg	Val	
				85					90					95		
aca	gtg	ctc	ggc	gcc	gca	ttc	aaa	ccc	aac	tcg	gac	gat	gtc	cgc	gat	336
Thr	Val	Leu	Gly	Ala	Ala	Phe	Lys	Pro	Asn	Ser	Asp	Asp	Val	Arg	Asp	
			100					105					110			
tct	ccg	gcg	ctg	tcg	gtc	gcg	ggg	tcg	ctg	tcg	ctc	cag	ggg	gcg	gcg	384
Ser	Pro	Ala	Leu	Ser	Val	Ala	Gly	Ser	Leu	Ser	Leu	Gln	Gly	Ala	Ala	
			115				120						125			
gtc	tcg	gtc	tac	gac	ccg	gaa	gct	atg	gac	aac	gct	cga	cgc	gtc	ttc	432
Val	Ser	Val	Tyr	Asp	Pro	Glu	Ala	Met	Asp	Asn	Ala	Arg	Arg	Val	Phe	
	130					135					140					
ccg	acg	ctc	agc	tat	gcg	tcc	agc	act	aaa	gag	gcg	ctt	atc	gac	gcc	480
Pro	Thr	Leu	Ser	Tyr	Ala	Ser	Ser	Thr	Lys	Glu	Ala	Leu	Ile	Asp	Ala	
	145				150					155					160	
cac	ctc	gtc	gtt	ctt	gcc	act	gaa	tgg	caa	gaa	ttc	cgc	gac	ctt	gac	528
His	Leu	Val	Val	Leu	Ala	Thr	Glu	Trp	Gln	Glu	Phe	Arg	Asp	Leu	Asp	
				165				170						175		
ccc	gaa	gtg	gcg	gga	ggg	gtc	gtc	gag	aag	cgc	gct	att	att	gat	ggc	576
Pro	Glu	Val	Ala	Gly	Gly	Val	Val	Glu	Lys	Arg	Ala	Ile	Ile	Asp	Gly	
			180					185					190			
cga	aac	gtc	ctc	gat	gtt	gcc	aaa	tgg	aag	gcc	gcc	ggg	tgg	gaa	atg	624
Arg	Asn	Val	Leu	Asp	Val	Ala	Lys	Trp	Lys	Ala	Ala	Gly	Trp	Glu	Met	
			195				200					205				
gaa	gcg	ctc	ggc	cgc	aac	ctt	tagtg	cggtg	gatc	aggcgg	ggc					668
Glu	Ala	Leu	Gly	Arg	Asn	Leu										
	210					215										

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Ala	Val	Ala	Glu	Ile	Cys	Glu	Pro	Thr	Gly	Ala	Asp	Ala	Val	Ala	Leu	
1				5					10					15		

Val	Asp	Ala	Ile	Gly	His	Asp	Asp	Arg	Ile	Gly	Arg	Lys	Phe	Leu	Gly	
	20							25					30			

Ala	Gly	Leu	Gly	Phe	Gly	Gly	Gly	Cys	Leu	Pro	Lys	Asp	Ile	Arg	Ala	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

[illegible]

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
40 45 50	
ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

<210> 264
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
 Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
 1 5 10 15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
 20 25 30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
 325 330 335
 Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
 340 345 350
 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 355 360 365

<210> 265

<211> 1124

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1101)

<223> RXA01216

<400> 265

acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca 48
 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
 1 5 10 15

acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
 20 25 30

ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu	
35 40 45	
caa aaa gat gct tca gca gaa gtc caa gcc atc gat gag gtc aac tcc	192
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser	
50 55 60	
ggt gtc ttt gct ttc gac gcc gcc atc ttg cgt tcc gca ctg gct gaa	240
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu	
65 70 75 80	
ctg aag tcc gac aac gct cag ggc gag ctg tac ctg acc gac gtt ttg	288
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu	
85 90 95	
ggc att gct cgt ggc gag ggc cac cca gtg cgc gcc cac acc gcc gcc	336
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala	
100 105 110	
gat gct cgt gaa ctc gcc ggc gtc aac gat cgt gtg cag ctc gca gaa	384
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu	
115 120 125	
gcc ggc gcc gaa cta aac cgt cgc acc gtc atc gcc gct atg cgt ggt	432
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly	
130 135 140	
ggc gca acc atc gtt gat cca gca acc acc tgg atc gat gtg gag gtt	480
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val	
145 150 155 160	
tct atc gga cgc gac gtg atc atc cac cct ggc acc cag ctc aag ggc	528
Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly	
165 170 175	
gaa act gtc atc gga gac cgc gtt gaa gtt ggt cca gac acc acc ttg	576
Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu	
180 185 190	
acc aac atg acc atc ggc gac ggc gca tcc gta atc cgc acc cac ggt	624
Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly	
195 200 205	
ttc gac tcc acc atc ggt gaa aac gcc acc gtt ggc ccc ttc acc tac	672
Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr	
210 215 220	
atc cgc cca gga acc aca ctg gga cca gaa ggc aag ctc ggt ggc ttc	720
Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe	
225 230 235 240	
gta gaa acc aag aag gcc aca atc ggc cgt ggc tcc aag gtt cca cac	768
Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His	
245 250 255	
ctc acc tat gtc ggc gac gcc acc atc ggc gag gaa tcc aac atc gga	816
Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly	
260 265 270	
gcc tcc tct gtc ttc gtg aac tac gac ggt gaa aac aag cac cac acc	864
Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr	

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct			912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala			
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124

<210> 266

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro	
1 5 10 15	

Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr	
20 25 30	

Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu	
35 40 45	

Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser	
50 55 60	

Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu	
65 70 75 80	

Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu	
85 90 95	

Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala	
100 105 110	

Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu	
115 120 125	

Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly	
130 135 140	

Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val	
145 150 155 160	

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175
 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190
 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205
 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220
 Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240
 Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255
 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270
 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285
 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300
 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
 305 310 315 320
 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
 325 330 335
 Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
 340 345 350
 Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
 355 360 365

<210> 267

<211> 981

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> RXA01259

<400> 267

aagagaatta tttctaaaat tcggtatcgt ctaagaaatg agtttgccaa tagctcagca 60

tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115
 Met Gly Thr Arg Phe
 1 5

ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
 10 15 20

acc	ccg	ggt	att	gaa	ctt	gtt	gcc	aaa	gag	gct	gct	gat	ctt	ggt	gca	211
Thr	Pro	Gly	Ile	Glu	Leu	Val	Ala	Lys	Glu	Ala	Ala	Asp	Leu	Gly	Ala	
			25					30						35		
act	cgg	tta	gca	att	atc	act	gct	ccg	aac	aaa	gac	gga	att	ctt	aaa	259
Thr	Arg	Leu	Ala	Ile	Ile	Thr	Ala	Pro	Asn	Lys	Asp	Gly	Ile	Leu	Lys	
		40					45					50				
cac	ttc	gag	gag	ttc	cct	gag	ctt	gag	gca	act	ctt	gag	gct	cgc	ggt	307
His	Phe	Glu	Glu	Phe	Pro	Glu	Leu	Glu	Ala	Thr	Leu	Glu	Ala	Arg	Gly	
	55					60					65					
aag	act	gat	caa	ctg	aat	aaa	gtt	cga	gca	gct	cga	gaa	ttg	att	gca	355
Lys	Thr	Asp	Gln	Leu	Asn	Lys	Val	Arg	Ala	Ala	Arg	Glu	Leu	Ile	Ala	
	70				75				80						85	
aca	gtt	cca	gtg	gtt	caa	gaa	aag	cca	ttg	ggg	ctt	ggt	cac	gct	gtt	403
Thr	Val	Pro	Val	Val	Gln	Glu	Lys	Pro	Leu	Gly	Leu	Gly	His	Ala	Val	
				90				95						100		
ggc	ctt	gct	gag	tct	gtg	ctc	gat	gat	gat	gaa	gat	gtt	gtg	gct	gtc	451
Gly	Leu	Ala	Glu	Ser	Val	Leu	Asp	Asp	Asp	Glu	Asp	Val	Val	Ala	Val	
			105					110					115			
atg	ctg	cca	gac	gat	ttg	gtg	ctg	cca	ttt	ggt	gtg	acc	gag	aga	atg	499
Met	Leu	Pro	Asp	Asp	Leu	Val	Leu	Pro	Phe	Gly	Val	Thr	Glu	Arg	Met	
		120					125					130				
gca	gaa	gtt	cgc	gct	aag	ttt	ggc	gga	tct	gtt	ctt	gca	gca	att	gag	547
Ala	Glu	Val	Arg	Ala	Lys	Phe	Gly	Gly	Ser	Val	Leu	Ala	Ala	Ile	Glu	
	135					140					145					
gtg	gct	gaa	gat	gaa	gtc	tca	aat	tac	gga	gta	ttt	aag	ctc	ggt	gaa	595
Val	Ala	Glu	Asp	Glu	Val	Ser	Asn	Tyr	Gly	Val	Phe	Lys	Leu	Gly	Glu	
	150				155				160						165	
ctc	gat	gca	gag	tcc	gaa	agt	gaa	ggc	att	agg	cgt	gtt	gta	gga	atg	643
Leu	Asp	Ala	Glu	Ser	Glu	Ser	Glu	Gly	Ile	Arg	Arg	Val	Val	Gly	Met	
				170				175						180		
gtt	gaa	aag	cct	gcg	cct	gaa	gat	gca	cca	tca	agg	ttt	gcc	gca	acg	691
Val	Glu	Lys	Pro	Ala	Pro	Glu	Asp	Ala	Pro	Ser	Arg	Phe	Ala	Ala	Thr	
			185					190					195			
ggc	cgt	tat	cta	ctt	gat	cga	gct	att	ttt	gat	gca	ctg	cgt	cga	att	739
Gly	Arg	Tyr	Leu	Leu	Asp	Arg	Ala	Ile	Phe	Asp	Ala	Leu	Arg	Arg	Ile	
		200					205					210				
gag	cct	ggt	gct	ggt	gga	gaa	ctg	caa	tta	aca	gat	gcc	atc	gca	tta	787
Glu	Pro	Gly	Ala	Gly	Gly	Glu	Leu	Gln	Leu	Thr	Asp	Ala	Ile	Ala	Leu	
	215					220					225					
ttg	atc	gaa	gaa	ggc	cat	ccg	gta	cac	att	gtg	gtt	cat	gaa	gga	aag	835
Leu	Ile	Glu	Glu	Gly	His	Pro	Val	His	Ile	Val	Val	His	Glu	Gly	Lys	
	230				235					240					245	
cgc	cat	gac	ctt	ggt	aat	cca	gct	ggg	tac	att	cct	gct	gtt	gtg	tac	883
Arg	His	Asp	Leu	Gly	Asn	Pro	Ala	Gly	Tyr	Ile	Pro	Ala	Val	Val	Tyr	
				250				255						260		
ttc	gga	ctt	cgt	cat	gca	gag	tac	ggt	tcc	aag	att	cac	cgt	gcg	gtg	931

Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
 1 5 10 15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240

Val	His	Glu	Gly	Lys	Arg	His	Asp	Leu	Gly	Asn	Pro	Ala	Gly	Tyr	Ile
				245					250					255	
Pro	Ala	Val	Val	Tyr	Phe	Gly	Leu	Arg	His	Ala	Glu	Tyr	Gly	Ser	Lys
			260					265					270		
Ile	His	Arg	Ala	Val	Lys	Glu	Ile	Leu	Ala	Glu	Phe	Glu	Ser		
		275					280					285			

```
<210> 269
<211> 526
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(526)
<223> RYA02028
```

<400> 269																	
ctgcgcagttc ctgcttagtt tggctcataa atctaaggat aaccggttatt ttcggagggg																	60
tacgacgatt ggggttgcg gggcaggtac tcttggttcc																	
Met Ser Leu Pro Ile																	115
1 5																	
gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga																	163
Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly																	
10 15 20																	
ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg																	211
Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu																	
25 30 35																	
ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct																	259
Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala																	
40 45 50																	
gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa																	307
Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys																	
55 60 65																	
gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg																	355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr																	
70 75 80 85																	
ctg atg gag cgt gcc aag act gac cag gtg gag ata atc cgc cgc gcc																	403
Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala																	
90 95 100																	
gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg																	451
Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly																	
105 110 115																	
cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa																	499
Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu																	
120 125 130																	
gat gtc gta gcg gtg atg ttg ccg cac																	526
Asp Val Val Ala Val Met Leu Pro His																	

135

140

<210> 270

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
 1 5 10 15

Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
 20 25 30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
 35 40 45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
 50 55 60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65 70 75 80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
 85 90 95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
 100 105 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
 115 120 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
 130 135 140

<210> 271

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXA01262

<400> 271

tatactcgtc aagggccttc gataaaacaa agacaatttt ccccgacgg gacaatctga 60

aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
 Met Lys Ile Ala Val
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
 10 15 20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
 25 30 35

gtt caa gaa ttt cgt tcg cca att gtc gat agc gat ctc gaa gaa tat	259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr	
40 45 50	
ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc	307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala	
55 60 65	
gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac	355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr	
70 75 80 85	
gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att	403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile	
90 95 100	
gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg	451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser	
105 110 115	
act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa	499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu	
120 125 130	
gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc	547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe	
135 140 145	
tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	

[illegible]

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
1 5 10 15

Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
20 25 30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
35 40 45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
50 55 60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
65 70 75 80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
85 90 95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
100 105 110

Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
 275 280 285
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
 290 295 300
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
 305 310 315 320
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
 325 330 335
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
 340 345 350
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
 355 360 365
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
 370 375 380
 Gln Arg Asp
 385

<210> 273

<211> 1209

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA01377

Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
 215 220 225

agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
 230 235 240 245

tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883
 Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
 250 255 260

gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
 265 270 275

cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
 280 285 290

ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
 295 300 305

att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
 310 315 320 325

atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
 330 335 340

ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171
 Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg
 345 350 355

ttt tcg tct gat cag taggcatttt tagccctttt gga 1209
 Phe Ser Ser Asp Gln
 360

<210> 274

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val
 1 5 10 15

Gly Gly Lys Gly Thr Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys
 20 25 30

Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
 35 40 45

Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
 50 55 60

Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
 65 70 75 80

Leu	Glu	Ile	Glu	Tyr	Val	Val	Glu	Asp	Gln	Pro	Leu	Gly	Thr	Gly	Gly	
				85					90					95		
Gly	Ile	Arg	Asn	Val	Tyr	Asp	Lys	Leu	Arg	His	Asp	Thr	Ala	Ile	Val	
				100					105					110		
Phe	Asn	Gly	Asp	Val	Leu	Ser	Gly	Ala	Asp	Leu	Asn	Ser	Ile	Leu	Asp	
				115					120					125		
Thr	His	Arg	Glu	Lys	Asp	Ala	Asp	Leu	Thr	Met	His	Leu	Val	Arg	Val	
				130					135					140		
Ala	Asn	Pro	Arg	Ala	Phe	Gly	Cys	Val	Pro	Thr	Asp	Glu	Asp	Gly	Arg	
				145					150					155		
Val	Ser	Glu	Phe	Leu	Glu	Lys	Thr	Glu	Asp	Pro	Pro	Thr	Asp	Gln	Ile	
				165					170					175		
Asn	Ala	Gly	Cys	Tyr	Val	Phe	Lys	Lys	Glu	Leu	Ile	Glu	Gln	Ile	Pro	
				180					185					190		
Ala	Gly	Arg	Ala	Val	Ser	Val	Glu	Arg	Glu	Thr	Phe	Pro	Gln	Leu	Leu	
				195					200					205		
Glu	Glu	Gly	Lys	Arg	Val	Phe	Gly	His	Val	Asp	Ala	Ser	Tyr	Trp	Arg	
				210					215					220		
Asp	Met	Gly	Thr	Pro	Ser	Asp	Phe	Val	Arg	Gly	Ser	Ala	Asp	Leu	Val	
				225					230					235		
Arg	Gly	Ile	Ala	Tyr	Ser	Pro	Leu	Leu	Glu	Gly	Lys	Thr	Gly	Glu	Ser	
				245					250					255		
Leu	Val	Asp	Ala	Ser	Ala	Gly	Val	Arg	Asp	Gly	Val	Leu	Leu	Leu	Gly	
				260					265					270		
Gly	Thr	Val	Val	Gly	Arg	Gly	Thr	Glu	Ile	Gly	Ala	Gly	Cys	Arg	Val	
				275					280					285		
Asp	Asn	Thr	Val	Ile	Phe	Asp	Gly	Val	Thr	Ile	Glu	Pro	Gly	Ala	Val	
				290					295					300		
Ile	Glu	Asn	Ser	Ile	Ile	Ser	Ser	Gly	Ala	Arg	Ile	Gly	Ala	Asn	Ala	
				305					310					315		
His	Ile	Ser	Gly	Cys	Ile	Ile	Gly	Glu	Gly	Ala	Gln	Val	Gly	Ala	Arg	
				325					330					335		
Cys	Glu	Leu	Asn	Ala	Gly	Met	Arg	Val	Phe	Pro	Gly	Val	Val	Ile	Pro	
				340					345					350		
Asp	Ser	Gly	Ile	Arg	Phe	Ser	Ser	Asp	Gln							
				355					360							

<210> 275

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

```

accgaaatgg gggcattaata aggggctatc attcggaccc caaaacgatg tttagacaat 60

ttgttaccca gctttcatgc gggatagtta ttttgccttt atg gtt aag ggt gtg 115
                               Met Val Lys Gly Val
                               1 5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                               10 15 20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                               25 30 35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                               40 45 50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                               55 60 65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                               70 75 80 85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                               90 95 100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                               105 110 115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                               120 125 130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                               135 140 145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                               150 155 160 165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                               170 175 180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                               185 190 195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

```

200	205	210	
cag gcg ctg aaa gat gat gaa aat aac gag aac agt gat cat gac atg Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn Ser Asp His Asp Met 215 220 225			787
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val 230 235 240			835
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys 250 255 260			883
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His 265 270 275			931
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu 280 285 290			979
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe 295 300 305			1027
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile 310 315 320 325			1075
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val 330 335 340			1123
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val 345 350 355			1171
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn 360 365 370			1219
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp 375 380 385			1267
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys 390 395 400 405			1315
aac cag gta gtc taaacgggaa agggacctta aaa Asn Gln Val Val			1350

<210> 276

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
 1 5 10 15
 Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
 20 25 30
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
 35 40 45
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50 55 60
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65 70 75 80
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
 85 90 95
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
 100 105 110
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
 115 120 125
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
 130 135 140
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
 145 150 155 160
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
 165 170 175
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
 180 185 190
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
 195 200 205
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
 210 215 220
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
 225 230 235 240
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
 245 250 255
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
 260 265 270
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
 275 280 285
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
 290 295 300
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
 305 310 315 320
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

	325		330		335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val					
	340		345		350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala					
	355		360		365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val					
	370		375		380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val					
	385		390		395
Val Val Val Gly Lys Asn Gln Val Val					
	405				

<210> 277
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> RXN00014

<400> 277
 catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagtttag 60

tgagatctcc gaaacttta ggcactaga ctaacaacac atg agc aaa tat gca 115
 Met Ser Lys Tyr Ala
 1 5

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163
 Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
 10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
 Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
 25 30 35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259
 Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
 40 45 50

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307
 Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
 55 60 65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355
 Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
 70 75 80 85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403
 Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
 90 95 100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451
 Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile

105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175	180	
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190	195	
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
tagactcccg ggttttgctt ggt			903

<210> 278

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Met	Ser	Lys	Tyr	Ala	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Glu	Leu	Ala	Glu
1				5				10						15	

Leu	Ala	Asp	Ser	Ile	Thr	Leu	Asp	Arg	Phe	Glu	Ala	Ser	Asp	Leu	Glu
		20						25					30		

Val	Ser	Ser	Lys	Pro	Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala
		35					40					45			

Thr	Glu	Glu	Ala	Leu	Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp
	50					55				60					

Ser	Ile	Leu	Gly	Glu	Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg
65					70					75				80	

398

25								30				35				
gac	atg	act	ccc	gtc	agc	gat	gcc	gac	ctg	gcg	acc	gaa	gaa	gca	ctc	259
Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala	Thr	Glu	Glu	Ala	Leu	
40				45				50								
cgc	gag	aaa	atc	gcc	acc	gcc	cgc	ccc	gcc	gac	tcc	atc	ctc	ggt	gaa	307
Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp	Ser	Ile	Leu	Gly	Glu	
55				60				65								
gaa	ttc	ggt	ggc	gac	gta	gaa	ttc	agc	ggc	cgc	cag	tgg	atc	atc	gac	355
Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg	Gln	Trp	Ile	Ile	Asp	
70				75				80				85				
ccc	atc	gac	ggc	acc	aaa	aac	tac	gtc	cgc	ggc	gtc	ccc	gta	tgg	gca	403
Pro	Ile	Asp	Gly	Thr	Lys	Asn	Tyr	Val	Arg	Gly	Val	Pro	Val	Trp	Ala	
90				95				100								
acc	ctg	atc	gcg	ctg	ctc	gac	aac	ggc	aaa	ccc	gtc	gca	ggt	gtc	atc	451
Thr	Leu	Ile	Ala	Leu	Leu	Asp	Asn	Gly	Lys	Pro	Val	Ala	Gly	Val	Ile	
105				110				115								
tcc	gca	ccc	gca	ctg	gct	agg	cgt	tgg	tgg	gca	tcc	gaa	ggg	gcc	ggc	499
Ser	Ala	Pro	Ala	Leu	Ala	Arg	Arg	Trp	Trp	Ala	Ser	Glu	Gly	Ala	Gly	
120				125				130								
gca	tgg	cgc	acc	ttc	aac	ggc	agc	tcc	cca	cgc	aaa	ctg	tcc	gtg	tcc	547
Ala	Trp	Arg	Thr	Phe	Asn	Gly	Ser	Ser	Pro	Arg	Lys	Leu	Ser	Val	Ser	
135				140				145								
cag	gtg	tcc	aag	ctt	gac	gac	gcc	tcc	ctc	tcc	ttc	tcc	tcc	ctc	tcc	595
Gln	Val	Ser	Lys	Leu	Asp	Asp	Ala	Ser	Leu	Ser	Phe	Ser	Ser	Leu	Ser	
150				155				160				165				
ggc	tgg	gcc	gaa	cga	gat	ttg	cgc	gat	cag	ttc	gtc	tcc	cta	act	gat	643
Gly	Trp	Ala	Glu	Arg	Asp	Leu	Arg	Asp	Gln	Phe	Val	Ser	Leu	Thr	Asp	
170				175				180								
acc	acc	tgg	cga	ctc	cgc	ggc	tac	ggc	gac	ttc	ttc	tcc	tac	tgc	ctc	691
Thr	Thr	Trp	Arg	Leu	Arg	Gly	Tyr	Gly	Asp	Phe	Phe	Ser	Tyr	Cys	Leu	
185				190				195								
gtc	gcc	gaa	ggt	gcc	gtc	gat	atc	gcc	gct	gaa	cca	gaa	gtc	agc	ctc	739
Val	Ala	Glu	Gly	Ala	Val	Asp	Ile	Ala	Ala	Glu	Pro	Glu	Val	Ser	Leu	
200				205				210								
tgg	gat	ctt	gct	ccc	ctg	tcc	atc	ctg	gtc	acc	gaa	gcc	gga	gga	aag	787
Trp	Asp	Leu	Ala	Pro	Leu	Ser	Ile	Leu	Val	Thr	Glu	Ala	Gly	Gly	Lys	
215				220				225								
ttc	acc	tca	ctg	gct	ggc	gtc	gat	gga	cca	cac	ggt	ggc	gat	gca	gta	835
Phe	Thr	Ser	Leu	Ala	Gly	Val	Asp	Gly	Pro	His	Gly	Gly	Asp	Ala	Val	
230				235				240				245				
gcc	acc	aac	ggc	atc	ctg	cac	gat	gag	acg	ctg	gat	cgt	tta	aaa		880
Ala	Thr	Asn	Gly	Ile	Leu	His	Asp	Glu	Thr	Leu	Asp	Arg	Leu	Lys		
250				255				260								
tagactcccg gggttttgctt ggt																903

<210> 280
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280

```

Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
 1           5           10           15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
          20           25           30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
      35           40           45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
 50           55           60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
 65           70           75           80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
          85           90           95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
      100           105           110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
      115           120           125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
      130           135           140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
      145           150           155           160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
          165           170           175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
      180           185           190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
      195           200           205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
      210           215           220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
      225           230           235           240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
          245           250           255

Asp Arg Leu Lys
      260

```

<210> 281
 <211> 978
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01570

<400> 281

```

cactgaactc cgttttggat ctcggaacaa tcgaagccac cggatttagc gcaccgacct 60
ggcagaccgc cctcaacgac tacctcaagg aactotcaaa gtg aaa ggc atc atc 115
                                   Val Lys Gly Ile Ile
                                   1 5

ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
                                   10 15 20

tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                                   25 30 35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
                                   40 45 50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
                                   55 60 65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
                                   70 75 80 85

cta gcc caa gca ttc atc atc gcc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
                                   90 95 100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
                                   105 110 115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
                                   120 125 130

tat gag gtc tcc gat cct gag cgt tat gcc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
                                   135 140 145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
                                   150 155 160 165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
                                   170 175 180

atc gcc aag tca atc aag cct tcc tcg cgt gcc gaa ctg gaa atc acc 691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
                                   185 190 195

```

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggttgag gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
 280 285

<210> 282

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
 1 5 10 15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
 20 25 30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
 130 135 140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
 145 150 155 160

Thr	Ala	Pro	Lys	Ser	Asn	Phe	Ala	Val	Val	Gly	Leu	Tyr	Phe	Tyr	Asp
				165					170					175	
Asn	Arg	Val	Val	Asp	Ile	Ala	Lys	Ser	Ile	Lys	Pro	Ser	Ser	Arg	Gly
			180					185					190		
Glu	Leu	Glu	Ile	Thr	Ser	Val	Asn	Asp	Ala	Tyr	Leu	Gln	Gln	Gly	Ala
		195					200					205			
Leu	Thr	Val	Gln	Arg	Leu	Asp	Arg	Gly	Asp	Val	Trp	Leu	Asp	Thr	Gly
	210					215					220				
Thr	Ile	Asp	Ser	Met	Ser	Glu	Ala	Ser	Ser	Tyr	Val	Glu	Val	Leu	Gln
225					230					235					240
Lys	Arg	Thr	Gly	Asn	Ile	Ile	Gly	Ser	Pro	Glu	Val	Ala	Ala	Tyr	Arg
				245					250					255	
Glu	Gly	Phe	Ile	Thr	Ala	Glu	Glu	Leu	Thr	Val	Leu	Gly	Glu	Glu	Leu
			260					265					270		
Lys	Lys	Ser	Gly	Tyr	Gly	Asn	Tyr	Leu	Leu	Arg	Ala	Leu			
		275					280					285			

<210> 283

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (868)

<223> RXA02666

<400> 283

gctcggcgac	gaggaagaga	agaaggacgc	attcgacgac	ttcgacgatt	ccgacgtgga	60										
tcttgacgat	ctgagcttcg	acgacgaaga	ttagacgccc	atg	tcg	tct	aca	cga	115							
				Met	Ser	Ser	Thr	Arg								
				1				5								
atc	ccc	gtc	atc	gca	ctc	ctc	gcg	gcg	gcg	ggg	cgc	gga	acc	cgc	ctc	163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10					15					20		
ggc	gga	ccc	atc	ccc	aaa	gca	ttc	gtc	acg	ttg	cgt	gaa	cgc	aca	ctt	211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			
tta	gag	cgc	tcg	ctc	caa	gcc	atg	ctc	acc	tcc	gaa	agc	gtc	gac	gaa	259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
		40					45					50				
atc	atc	atc	ctc	gtc	agc	ccc	gac	atg	gaa	acc	tac	gcc	cgc	gat	ttg	307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
	55					60					65					
ctg	cgc	aaa	cgc	ggt	ctt	ttg	aac	gac	ccc	gaa	ggg	gta	cgc	gta	cgg	355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	

70	75	80	85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt				403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891
<210> 284				
<211> 256				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 284				
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly	1	5	10	15
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu	20	25	30	

405

	1	5	
acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc			163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile	10	15	20
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc			211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg	25	30	35
ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg			259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val	40	45	50
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac			307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His	55	60	65
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac			355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His	70	75	80
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc			403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr	90	95	100
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc			451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val	105	110	115
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca			499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro	120	125	130
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc			547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser	135	140	145
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc			595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly	150	155	160
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa			643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln	170	175	180
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt			691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu	185	190	195
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc			739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg	200	205	210
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct			787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser	215	220	225
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa			835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu	230	235	240
			245

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
 250 255 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
 265 270 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
 280 285 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 286

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
 1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 287
 <211> 1134
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> RXA01887

<400> 287
 catctttaca ggaaaccctt tgacggcatc aatgggtggt atctagtatc tactagaacg 60
 ttatagtaga acgttctagt aaaacttggg aggatgaaaa atg tca gtc aaa ctt 115
 Met Ser Val Lys Leu
 1 5
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile
 10 15 20
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr
 25 30 35
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser
 40 45 50
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile
 55 60 65

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
70 75 80 85	
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
 330 335

ttttaaaactc gca 1134

<210> 288

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn
 1 5 10 15

His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80

Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125

Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
 195 200 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220

Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240

[illegible]

```
<210> 289
<211> 996
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(973)  
<223> RXN00013
```

<400> 289																	
ctgcagaaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcttaga 60																	
acgccacctt attcagcaca cttggccgac ggcattgcaca atg gaa ggc atg act 115																	
													Met	Glu	Gly	Met	Thr
													1				5
aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163																	
Asn		Pro		Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu	Glu	Asp	Met	Ile	Lys
					10							15		20			
acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211																	
Thr		Ile	Thr		Lys	Thr	Phe	Val	Ile	Ala	His	Asp	Gln	Asp	Ser	Asp	Glu
					25							30		35			
cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259																	
His		Leu		Ala	Gln	Ala	Leu	Val	Tyr	Asn	Ala	Gly	Arg	Leu	Ala	Trp	Arg
					40							45		50			
atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307																	
Met		Arg		Glu	Asn	Gly	Val	Asp	Thr	Asp	Tyr	Lys	Thr	Ser	Val	Ser	Asp
					55							60		65			
gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355																	
Val		Val		Thr	Asp	Ala	Asp	Arg	Ala	Ala	Glu	Ala	Phe	Val	Ala	Gly	Val
70							75							80		85	
ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403																	
Leu		Glu	Ala	Leu	Arg	Pro	Glu	Asp	Gly	Val	Leu	Gly	Glu	Glu	Gly	Ala	

90	95	100	
gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat			451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp			
105	110	115	
ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc			499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu			
120	125	130	
gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc			547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly			
135	140	145	
gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga			595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly			
150	155	160	165
atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc			643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala			
170	175	180	
ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc			691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile			
185	190	195	
gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct			739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro			
200	205	210	
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
215	220	225	
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
230	235	240	245
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
250	255	260	
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
265	270	275	
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
280	285	290	
taacaacaca tgagcaaata tgc			996

<210> 290

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
 165 170 175
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
 180 185 190
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
 195 200 205
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
 210 215 220
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
 225 230 235 240
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
 245 250 255
 Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
 260 265 270
 Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
 275 280 285
 Ala Leu Asp
 290

<210> 291

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00013

<400> 291

ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act 115
 Met Glu Gly Met Thr
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
 90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
 Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
 105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
 Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
 120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
 Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
 135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
 Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
 150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
 Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
 170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
 Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
 185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
 280 285 290

tagcaacaca tgagcaaata tgc 996

<210> 292
 <211> 291
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 292
 Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160

[illegible]

```
<210> 293
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(925)  
<223> RXA01099
```

```

<400> 293
ggatgagggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagaggct ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg 115
Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

```

gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc 355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
70 75 80 85

aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
90 95 100

gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
105 110 115

aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
120 125 130

cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
135 140 145

ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
150 155 160 165

cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
170 175 180

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
185 190 195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
200 205 210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
215 220 225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
230 235 240 245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
250 255 260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
265 270 275

taaaatgggc gtggcaattc gag 948

<210> 294

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

```

Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
 1           5           10           15

Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
          20           25           30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
          35           40           45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
 50           55           60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65           70           75           80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
          85           90           95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
          100          105          110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
          115          120          125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
          130          135          140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
          145          150          155          160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
          165          170          175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
          180          185          190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
          195          200          205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
          210          215          220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
          225          230          235          240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
          245          250          255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
          260          265          270

Glu Tyr Lys
          275

```

<210> 295

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(576)
 <223> RXN01332

<400> 295

```

cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct   48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
  1             5             10             15

gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct   96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
             20             25             30

atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag   144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
             35             40             45

ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc   192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
             50             55             60

ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc   240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
             65             70             75             80

gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc   288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
             85             90             95

atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa   336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
             100             105             110

tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac   384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
             115             120             125

cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc   432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
             130             135             140

gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt   480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
             145             150             155             160

gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc   528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
             165             170             175

ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg   576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
             180             185             190

```

<210> 296
 <211> 192
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
 1 5 10 15
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
 20 25 30
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
 35 40 45
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
 50 55 60
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65 70 75 80
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
 85 90 95
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
 100 105 110
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
 115 120 125
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
 130 135 140
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
 145 150 155 160
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
 165 170 175
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
 180 185 190

<210> 297

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(549)

<223> FRXA01332

<400> 297

gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
 Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15

ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
 20 25 30

ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
85	90	95	
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
100	105	110	
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
115	120	125	
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
130	135	140	
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
145	150	155	160
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
165	170	175	
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
180			

<210> 298

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15

Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
 20 25 30

Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala
 35 40 45

Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
 50 55 60

Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys
 65 70 75 80

Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn

	85		90		95
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met					
	100		105		110
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln					
	115		120		125
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro					
	130		135		140
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys					
	145		150		155
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile					
	165		170		175
Met Glu Leu Glu Asn Gly Val					
	180				

<210> 299
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA01632

<400> 299
 aagggtgca acgtgctttc gacaccacca tcgcagcggt tgaacaagct gctcgtctcg 60
 cccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115
 Met Thr Leu Arg Ile
 1 5
 gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163
 Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
 10 15 20
 gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211
 Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile
 25 30 35
 gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259
 Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
 40 45 50
 tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307
 Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
 55 60 65
 ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355
 Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
 70 75 80 85
 cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403
 Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
 90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val	
330 335	

cct

1128

<210> 300

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val
 1 5 10 15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile
 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
 100 105 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
 115 120 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
 130 135 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
 145 150 155 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
 165 170 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
 180 185 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
 195 200 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
 210 215 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
 225 230 235 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
 245 250 255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

275						280						285					
Ala	Thr	Phe	Ala	Gln	Gly	Ile	Arg	Asp	Gly	Gln	Gly	Phe	Ser	Pro	Asn		
290						295						300					
Phe	Glu	Asp	Gly	Val	Ile	Ala	Leu	Glu	Leu	Ala	Asn	Ala	Cys	Leu	Glu		
305						310						315					
Ser	Ala	Gln	Thr	Gly	Arg	Thr	Val	Thr	Leu	Asn	Pro	Ala	Asn	Val			
325						330						335					

```
<210> 301
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1183)  
<223> RXA01633
```

<400> 301															
gcgaatgcat	gccttgaatc	agctcaaacc	ggccgcaccg	tcacctcaa	ccctgccaac	60									
gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115															
Met Lys Asn Ile Thr 5															
1															
atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac 163															
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn 20															
10 15															
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag 211															
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu 35															
25 30															
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg 259															
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala 50															
40 45 50															
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac 307															
Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp 65															
55 60															
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat 355															
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp 85															
70 75 80															
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag 403															
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys 100															
90 95 100															
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att 451															
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile 115															
105 110 115															
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac 499															
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp 130															
120 125 130															

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly 135 140 145	547
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro 150 155 160 165	595
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu 170 175 180	643
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu 185 190 195	691
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val 200 205 210	739
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr 215 220 225	787
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val 230 235 240 245	835
cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp 250 255 260	883
gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr 265 270 275	931
ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys 280 285 290	979
aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn 295 300 305	1027
cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala 310 315 320 325	1075
gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val 330 335 340	1123
cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu 345 350 355	1171
gtt cca tct gct taaaacctta ctgcttatct aaa Val Pro Ser Ala 360	1206

<210> 302
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 302

Met	Lys	Asn	Ile	Thr	Ile	Gly	Met	Val	Gly	Val	Gly	Arg	Ile	Gly	Arg
1				5					10					15	
Met	His	Val	Ala	Asn	Met	Leu	Ala	Val	Ala	Glu	Thr	Leu	Lys	Glu	Arg
			20					25					30		
Asp	Leu	Asn	Ile	Glu	Ile	Val	Leu	Ala	Asp	Ala	Met	Pro	Gly	Phe	Ala
		35					40					45			
Glu	Gln	Val	Gly	Ala	Asp	Met	Gly	Val	Lys	Ala	Ala	Ala	Ser	Val	Asp
	50					55					60				
Lys	Leu	Ile	Glu	Asp	Gly	Val	Asp	Ala	Leu	Phe	Ile	Ala	Thr	Ser	Thr
65					70					75					80
Ala	Gly	His	Val	Asp	Val	Leu	Arg	Lys	Gly	Ile	Ala	Ala	Lys	Leu	Pro
				85					90					95	
Met	Phe	Cys	Glu	Lys	Pro	Ile	Ala	Ser	Asp	Val	Pro	Glu	Ser	Leu	Asn
			100					105					110		
Ile	Ile	Arg	Glu	Ile	Asp	Ala	Ala	Gly	Ala	Thr	Val	Gln	Val	Gly	His
		115					120					125			
Gln	Arg	Arg	Phe	Asp	Leu	Gly	Tyr	Gln	Glu	Ala	Lys	Arg	Arg	Leu	Asp
	130					135					140				
Ala	Gly	Asp	Leu	Gly	Trp	Leu	His	Ser	Leu	Lys	Ala	Val	Ser	Ser	Asp
145					150					155					160
Ala	Phe	Pro	Pro	Pro	Val	Ser	Tyr	Cys	Ala	Thr	Ser	Gly	Gly	Leu	Phe
				165					170					175	
Arg	Asp	Val	Ser	Leu	His	Asp	Phe	Asp	Ile	Ile	Arg	Trp	Leu	Thr	Gly
			180					185					190		
Gln	Asp	Ile	Val	Glu	Val	Tyr	Ala	Lys	Gly	Ser	Asn	Asn	Gly	Asp	Pro
	195						200					205			
Glu	Ile	Gly	Ala	Val	Gly	Asp	Ile	Asp	Thr	Gly	Ala	Ala	Leu	Leu	Thr
	210					215					220				
Leu	Ala	Asp	Gly	Thr	Leu	Ala	Thr	Ala	Ile	Ala	Thr	Arg	Tyr	Asn	Gly
225					230					235					240
Ala	Gly	His	Asp	Val	Arg	Leu	Asp	Val	Met	Gly	Ser	Lys	Asp	Ser	Thr
			245						250					255	
Ile	Val	Gly	Leu	Asp	Glu	Lys	Ser	Ala	Phe	Ala	Ser	Ala	Glu	Glu	Gly
			260					265					270		
Ile	Asp	Phe	Pro	Thr	Gly	Glu	Ser	His	Pro	Thr	Phe	Ala	Glu	Arg	Phe
	275						280					285			
Ala	Asp	Ala	Tyr	Lys	Asn	Glu	Cys	Ile	Ala	Phe	Val	Glu	Leu	Ile	Leu

290					295					300					
Gly 305	Glu	Arg	Glu	Asn	Pro 310	Cys	Thr	Pro	Ala	Asp 315	Ala	Val	Ala	Ala	Ala 320
Ile	Val	Ala	Asp	Ala 325	Ala	Gln	Leu	Ser	Leu 330	Val	Thr	Gly	Glu	Pro 335	Val
Lys	Ile	Pro	Thr 340	Val	Arg	Glu	Ile	Leu 345	Glu	Gly	Ser	Ala	Gln 350	Pro	Val
Glu	Val	Arg 355	Ala	Leu	Val	Pro	Ser	Ala 360							

```
<210> 303
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1123)
<223> RXN01406
```

<400> 303																
gttcctcatt	cctctaatacg	gcgcactatc	tttgcctcgc	gacggcggtg	cccgagcctt	60										
ttcctcctct	tagaaaccca	cttctgaaag	gtataaaaac	atg	act	att	cga	atc	115							
				Met	Thr	Ile	Arg	Ile								
				1				5								
gga	ctc	gtt	ggc	tac	ggg	gtc	ggc	ggc	agg	ctc	ttt	cac	acc	cct	tac	163
Gly	Leu	Val	Gly	Tyr	Gly	Val	Gly	Gly	Arg	Leu	Phe	His	Thr	Pro	Tyr	
				10					15					20		
atc	caa	gct	tct	acg	cac	tgc	gaa	tta	gta	ggc	gta	gtt	gct	cgt	tcc	211
Ile	Gln	Ala	Ser	Thr	His	Cys	Glu	Leu	Val	Gly	Val	Val	Ala	Arg	Ser	
			25					30					35			
gaa	ggc	acc	aaa	gca	gcc	gtt	gca	gaa	gat	ctt	cca	gat	gtt	gcc	atc	259
Glu	Gly	Thr	Lys	Ala	Ala	Val	Ala	Glu	Asp	Leu	Pro	Asp	Val	Ala	Ile	
		40					45					50				
gtg	gga	tcg	ctg	aca	gaa	ctc	ctc	gaa	ctg	ggc	gtc	gat	gca	gtg	gtg	307
Val	Gly	Ser	Leu	Thr	Glu	Leu	Leu	Glu	Leu	Gly	Val	Asp	Ala	Val	Val	
	55					60					65					
atc	tcc	acc	cct	cca	gcc	acg	cgc	cgg	gaa	ctg	gcc	ttg	gaa	gca	atc	355
Ile	Ser	Thr	Pro	Pro	Ala	Thr	Arg	Arg	Glu	Leu	Ala	Leu	Glu	Ala	Ile	
	70				75				80						85	
aac	gca	ggg	gtc	gca	gtg	gtt	gcc	gat	aaa	ccg	ttt	gca	cca	tca	gcc	403
Asn	Ala	Gly	Val	Ala	Val	Val	Ala	Asp	Lys	Pro	Phe	Ala	Pro	Ser	Ala	
				90					95					100		
gca	gat	gcc	atg	gaa	ctt	gtc	gaa	gcc	gcc	gaa	aag	gct	gga	gtg	ctg	451
Ala	Asp	Ala	Met	Glu	Leu	Val	Glu	Ala	Ala	Glu	Lys	Ala	Gly	Val	Leu	
			105					110					115			
ctc	aac	gtc	ttc	cac	aac	agg	cgc	aac	gac	acc	cac	att	gtc	acg	qca	499

Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala
 120 125 130
 ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga 547
 Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg
 135 140 145
 cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt 595
 Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly
 150 155 160 165
 ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc 643
 Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu
 170 175 180
 atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt 691
 Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu
 185 190 195
 cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa 739
 Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu
 200 205 210
 tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag 787
 Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu
 215 220 225
 tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac 835
 Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn
 230 235 240 245
 tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc 883
 Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr
 250 255 260
 aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc 931
 Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr
 265 270 275
 ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat 979
 Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp
 280 285 290
 tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc 1027
 Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly
 295 300 305
 gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg 1075
 Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu
 310 315 320 325
 gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc 1123
 Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser
 330 335 340
 taaggagaag tgctgctggc tgc 1146

<210> 304

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met	Thr	Ile	Arg	Ile	Gly	Leu	Val	Gly	Tyr	Gly	Val	Gly	Gly	Arg	Leu	1	5	10	15
Phe	His	Thr	Pro	Tyr	Ile	Gln	Ala	Ser	Thr	His	Cys	Glu	Leu	Val	Gly	20	25	30	
Val	Val	Ala	Arg	Ser	Glu	Gly	Thr	Lys	Ala	Ala	Val	Ala	Glu	Asp	Leu	35	40	45	
Pro	Asp	Val	Ala	Ile	Val	Gly	Ser	Leu	Thr	Glu	Leu	Leu	Glu	Leu	Gly	50	55	60	
Val	Asp	Ala	Val	Val	Ile	Ser	Thr	Pro	Pro	Ala	Thr	Arg	Arg	Glu	Leu	65	70	75	80
Ala	Leu	Glu	Ala	Ile	Asn	Ala	Gly	Val	Ala	Val	Val	Ala	Asp	Lys	Pro	85	90	95	
Phe	Ala	Pro	Ser	Ala	Ala	Asp	Ala	Met	Glu	Leu	Val	Glu	Ala	Ala	Glu	100	105	110	
Lys	Ala	Gly	Val	Leu	Leu	Asn	Val	Phe	His	Asn	Arg	Arg	Asn	Asp	Thr	115	120	125	
His	Ile	Val	Thr	Ala	Leu	Gly	Ile	Gln	Glu	Glu	Leu	Gly	Ala	Met	Arg	130	135	140	
Gly	Leu	Asp	Leu	Arg	Leu	Asp	Leu	Ile	Glu	Pro	Asp	Ser	Leu	Glu	Ala	145	150	155	160
Gly	Pro	Glu	Gly	Gly	Leu	Leu	Arg	Asp	Leu	Gly	Ser	His	Val	Val	Asp	165	170	175	
Gln	Thr	Leu	Val	Leu	Met	Gly	Pro	Ala	Thr	Ser	Val	Thr	Ala	Gln	Leu	180	185	190	
Gly	Ser	Ile	Asp	Leu	Pro	Glu	Gly	Pro	Thr	Asn	Ala	Arg	Phe	Arg	Ile	195	200	205	
Val	Leu	Glu	His	Glu	Ser	Gly	Ala	Val	Ser	His	Ile	Ser	Ala	Ser	Lys	210	215	220	
Ile	Asp	Arg	Leu	Glu	Ser	Trp	Glu	Ile	Arg	Leu	Val	Gly	Glu	Arg	Gly	225	230	235	240
Ser	Tyr	Val	Ser	Asn	Tyr	Thr	Asp	Val	Gln	Thr	Val	Ala	Ile	Lys	Gln	245	250	255	
Gly	Leu	Arg	Pro	Thr	Asn	Asp	Arg	Glu	His	Trp	Gly	Tyr	Glu	Ser	Glu	260	265	270	
Glu	Arg	Trp	Gly	Thr	Leu	Val	Thr	Asp	Glu	Gly	Ser	Lys	Val	Ile	Pro	275	280	285	
Ser	Ala	Gln	Gly	Asp	Tyr	Thr	Arg	Phe	Tyr	Asp	Ala	Phe	Ala	Leu	Ala	290	295	300	
Val	Glu	Asn	Gly	Gly	Ala	Gly	Pro	Val	Pro	Ala	Arg	Glu	Gly	Val	Ala				

```

305              310              315              320
Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg
              325              330              335
Thr Ile Glu Leu Ser
              340

```

```
<210> 305
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1177)  
<223> BXN01630
```

<400> 305																		
gtaggtgagt	cttcgtgaga	tacccccggc	cagtcataca	ggtcaaccaa	gctccaccac											60		
ccagataaaa acctgcgggt tgcgttttag gagaattccc						atg	agt	gat	caa	aaa						115		
						Met	Ser	Asp	Gln	Lys								
						1						5						
att	gtt	gtt	ggc	ctg	cta	ggc	atc	acc	cac	ccg	cat	gcg	tcg	gcg	cgg	163		
Ile	Val	Val	Gly	Leu	Leu	Gly	Ile	Thr	His	Pro	His	Ala	Ser	Ala	Arg			
				10					15					20				
gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211		
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala			
				25					30					35				
gat	act	gat	tcc	cgc	ctc	cag	tac	ttc	acc	gac	aaa	tat	gat	gtt	gaa	259		
Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu			
				40					45					50				
ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307		
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile			
		55					60					65						
atg	gtt	cac	tcc	aag	agc	aag	gac	atg	gtc	cct	cac	gcc	aag	cgc	gcg	355		
Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala			
70					75					80					85			
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403		
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr			
				90					95					100				
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451		
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro			
			105					110					115					
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499		
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val			
			120					125					130					
cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547		
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val			
		135					140					145						

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag	595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu	
150 155 160 165	
cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc	643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly	
170 175 180	
tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc	691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser	
185 190 195	
gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc	739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser	
200 205 210	
cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc	787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val	
215 220 225	
agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc	835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser	
230 235 240 245	
cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc	883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu	
250 255 260	
cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca	931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro	
265 270 275	
cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct	979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala	
280 285 290	
cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc	1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile	
295 300 305	
agc aac ttc cgc aca gaa atg cag ggc tgg gtg aat tcc att cgc act	1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr	
310 315 320 325	
gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc	1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg	
330 335 340	
att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta	1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val	
345 350 355	
aac atc taagaggagc actccatgaa acc	1200
Asn Ile	

<210> 306

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
 1 5 10 15
 His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
 20 25 30
 Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
 35 40 45
 Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50 55 60
 Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65 70 75 80
 His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
 85 90 95
 Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
 100 105 110
 Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
 115 120 125
 Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
 130 135 140
 Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
 145 150 155 160
 Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
 165 170 175
 Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
 180 185 190
 Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
 195 200 205
 Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
 210 215 220
 Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
 225 230 235 240
 Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
 245 250 255
 Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
 260 265 270
 Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
 275 280 285
 Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
 290 295 300
 Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val

305	310						315						320		
Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala	325						330						335		
Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn	340						345						350		
Gln Gly Ile Ser Val Asn Ile	355														

```
<210> 307
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1189)
<223> RXN00528
```

<400> 307																
ttctgctggg	aatccccaca	ttttggaacg	tagcgtcgat	aagcgtgcgg	cgaagctttt	60										
tcggtcgcgg	ccgttatctt	tttaagagga	gaaatttttag	atg	agc	acg	tcc	acc	115							
				Met	Ser	Thr	Ser	Thr	5							
				1												
atc	agg	gtt	gcc	att	gcc	gga	gtc	gga	aac	tgc	gcg	acc	tcc	ctc	att	163
Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys	Ala	Thr	Ser	Leu	Ile	20
				10					15							
cag	ggt	gtg	gaa	tat	tac	cga	aat	gcg	gat	cct	tcc	gaa	act	gtc	ccg	211
Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro	Ser	Glu	Thr	Val	Pro	35
			25					30					35			
ggg	ttg	atg	cac	gtc	aaa	ttc	ggg	gat	tac	cac	gtt	ggc	gac	att	gaa	259
Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His	Val	Gly	Asp	Ile	Glu	50
		40					45					50				
ttc	gtg	gcc	gcg	ttc	gac	gtc	gac	gcc	gaa	aaa	gta	ggc	atc	gat	ctt	307
Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys	Val	Gly	Ile	Asp	Leu	65
		55				60					65					
gcc	gac	gcc	acc	gag	gct	tca	caa	aac	tgc	act	atc	aaa	atc	gcc	gat	355
Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr	Ile	Lys	Ile	Ala	Asp	85
		70				75				80						
gtc	cca	cag	acc	ggc	atc	aac	gtg	ctg	cgt	ggc	ccg	act	ctc	gac	ggc	403
Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly	Pro	Thr	Leu	Asp	Gly	100
				90					95							
ctg	ggc	gat	cat	tac	cgc	gcg	acc	atc	gac	gag	tcc	acc	gcc	gag	cca	451
Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu	Ser	Thr	Ala	Glu	Pro	115
			105					110								
gtc	gac	gtt	gtc	cag	gcg	ctt	atc	gac	gca	aaa	gcc	gat	gtt	ttg	gtg	499
Val	Asp	Val	Val	Gln	Ala	Leu	Ile	Asp	Ala	Lys	Ala	Asp	Val	Leu	Val	130
		120					125									

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa	547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
135 140 145	
gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc	595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
150 155 160 165	
atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc	643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
170 175 180	
cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc	691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
185 190 195	
cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat	739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
200 205 210	
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg	787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
215 220 225	
ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca	835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac	883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
250 255 260	
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac	931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt	979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
280 285 290	
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
295 300 305	
gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat	1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
310 315 320 325	
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag	1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
330 335 340	
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag	1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
345 350 355	
gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg	1212
Ala Phe Ile Ile Glu Ala	
360	

<210> 308
 <211> 363
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308

```

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
 1           5           10           15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
      20           25           30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
      35           40           45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
      50           55           60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
      65           70           75           80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
      85           90           95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
      100          105          110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
      115          120          125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
      130          135          140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
      145          150          155          160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
      165          170          175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
      180          185          190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
      195          200          205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
      210          215          220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
      225          230          235          240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
      245          250          255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
      260          265          270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
      275          280          285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

```

290 295 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
 305 310 315 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
 325 330 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
 340 345 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
 355 360

<210> 309
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXN03057

<400> 309
 catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60

aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115
 Leu Ala Ser Asp Leu
 1 5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85

gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
 105 110 115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499

Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220

aca 795

<210> 310

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
 1 5 10 15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155 160
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170 175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185 190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
	195	200 205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
210	215	220

<210> 311
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> FRXA02902

<400> 311
 catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60
 aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115
 Leu Ala Ser Asp Leu
 1 5
 ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20
 aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35
 gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50
 gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65
 ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85
 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

```

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
      105                      110                      115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499
Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
      120                      125                      130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
      135                      140                      145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
      150                      155                      160                      165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
      170                      175                      180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
      185                      190                      195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
      200                      205                      210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
His Glu Ser Gly Val His Thr Ser Glu Val Ser
      215                      220

aca 795

<210> 312
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 312
Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
  1                      5                      10                      15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
      20                      25                      30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
      35                      40                      45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
      50                      55                      60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
      65                      70                      75                      80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
      85                      90                      95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

```

100	105	110
Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp		
115	120	125
Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp		
130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
165	170	175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
180	185	190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
195	200	205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
210	215	220

<210> 313

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXA00251

<400> 313

aaccagcggtt ttcagcgaga tactggacat atcaactaaa atccctgaat aaaacatcta 60

acatgggttt tatacagaaa attcatatga aaggttgatc atg aag aag aag att	115
Met Lys Lys Lys Ile	
1 5	

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa	163
Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys	
10 15 20	

gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag	211
Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu	
25 30 35	

cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc	259
His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser	
40 45 50	

gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa	307
Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys	
55 60 65	

aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt	355
---	-----

Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
 70 75 80 85
 gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
 Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
 90 95 100
 gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc 451
 Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
 105 110 115
 gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499
 Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
 120 125 130
 ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac 547
 Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
 135 140 145
 gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
 Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
 150 155 160 165
 ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
 Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
 170 175 180
 ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691
 Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
 185 190 195
 tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739
 Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
 200 205 210
 gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
 215 220 225
 gaa ctg gcg gac cgg aaa gat tagttctgagg gggcttcctg gcc 831
 Glu Leu Ala Asp Arg Lys Asp
 230 235

<210> 314

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Lys Lys Lys Ile Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly
 1 5 10 15
 Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu
 20 25 30
 Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
 35 40 45
 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
 50 55 60

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65 70 75 80
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
 85 90 95
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
 100 105 110
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
 115 120 125
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
 130 135 140
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
 145 150 155 160
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
 165 170 175
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
 180 185 190
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
 195 200 205
 Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
 210 215 220
 Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
 225 230 235

<210> 315
 <211> 1008
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(985)
 <223> RXN02654

<400> 315
 tattttcggga aatttatata gcaatcctcg aaatcctaataaagatccct tatcgtggga 60
 gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5
 aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20
 cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35
 ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala	
		40					45					50				
ctt	att	act	ggg	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala	
	55					60				65						
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu	
70					75				80					85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggg	caa	403
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln	
				90				95						100		
aaa	gct	ttt	tct	ttc	cct	ggg	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg	
			105				110						115			
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggg	ggc	cta	gac	atc	ttg	499
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu	
	120					125						130				
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggg	ttg	acc	gaa	att	547
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile	
135						140					145					
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggg	agt	595
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser	
150					155				160						165	
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser	
				170				175						180		
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu	
			185				190						195			
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly	
	200					205						210				
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala	
215					220						225					
cca	ggg	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggg	cag	cca	caa	835
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln	
230					235					240					245	
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggg	883
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly	
				250				255						260		
cac	cct	gtt	gag	ttg	gca	ggg	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu	
			265				270						275			
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggg	ggg	acg	ccc	979
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro	

280 285 290 1008

acc cca tagtcggtac aagcgggaatc act
 Thr Pro
 295

<210> 316
 <211> 295
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 316
 Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp
 1 5 10 15
 Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
 20 25 30
 Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
 35 40 45
 Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
 50 55 60
 Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285

Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 317
 <211> 1008
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(985)
 <223> FRXA02654

<400> 317
 tatttttcgga aatttatataca gcaatcctcg aaatcctaataaagatccct tatcgtggga 60

gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
 40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
 55 60 65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355
 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
 70 75 80 85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
 90 95 100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451
 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
 105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
 120 125 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcggaatc act			1008
Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met	Ile	Ser	Leu	Leu	Asn	Asp	Pro	Arg	Thr	Leu	Phe	Pro	Lys	Val	Asp
1				5					10					15	

Pro	Pro	Lys	Gln	Ser	Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser
			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35					40					45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270
 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285
 Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 319

<211> 1605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1582)

<223> RXN01049

<400> 319

aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60

 aagaatattc tttattagtc agacctttaa aggaaacott atg gga tca att cca 115
 Met Gly Ser Ile Pro

aca	atg	tcc	atc	cct	ttt	gat	gac	tca	cgt	gga	cct	tat	gtc	ctt	gct	163
Thr	Met	Ser	Ile	Pro	Phe	Asp	Asp	Ser	Arg	Gly	Pro	Tyr	Val	Leu	Ala	
				10					15					20		
atg	gat	att	ggg	tcc	act	gca	tca	cga	ggg	gga	ctt	tat	gat	gct	tcc	211
Met	Asp	Ile	Gly	Ser	Thr	Ala	Ser	Arg	Gly	Gly	Leu	Tyr	Asp	Ala	Ser	
				25					30					35		
ggc	tgc	cca	atc	aaa	ggc	acc	aag	cag	cgc	gaa	tcc	cat	gaa	ttc	acc	259
Gly	Cys	Pro	Ile	Lys	Gly	Thr	Lys	Gln	Arg	Glu	Ser	His	Glu	Phe	Thr	
				40					45					50		
acc	ggg	gag	ggc	gtt	tcc	acc	att	gat	gct	gac	cag	gtg	gtt	tcg	gag	307
Thr	Gly	Glu	Gly	Val	Ser	Thr	Ile	Asp	Ala	Asp	Gln	Val	Val	Ser	Glu	
				55					60					65		
atc	acc	tca	gtt	att	aat	ggc	att	ttg	aac	gcg	gct	gat	cat	cac	aac	355
Ile	Thr	Ser	Val	Ile	Asn	Gly	Ile	Leu	Asn	Ala	Ala	Asp	His	His	Asn	
				70					75					80		
atc	aaa	gat	cag	atc	gcc	gct	gtc	gcg	cta	gat	tct	ttt	gca	tcc	tca	403
Ile	Lys	Asp	Gln	Ile	Ala	Ala	Val	Ala	Leu	Asp	Ser	Phe	Ala	Ser	Ser	
				90					95					100		
tta	atc	ttg	gtc	gat	ggg	gaa	ggc	aat	gcg	ctc	acc	ccg	tgc	att	acc	451
Leu	Ile	Leu	Val	Asp	Gly	Glu	Gly	Asn	Ala	Leu	Thr	Pro	Cys	Ile	Thr	
				105					110					115		
tac	gcg	gat	tct	cgt	tct	gca	cag	tat	gtg	gag	cag	ctg	cgc	gcg	gaa	499
Tyr	Ala	Asp	Ser	Arg	Ser	Ala	Gln	Tyr	Val	Glu	Gln	Leu	Arg	Ala	Glu	
				120					125					130		
atc	gat	gag	aag	gcc	tac	cac	ggc	cgc	acc	ggc	gtc	tgc	ttg	cac	acc	547
Ile	Asp	Glu	Lys	Ala	Tyr	His	Gly	Arg	Thr	Gly	Val	Cys	Leu	His	Thr	
				135					140					145		
tcc	tac	cac	cca	tcg	cgc	ttg	ctg	tgg	ctg	aaa	act	gag	ttc	gag	aaa	595
Ser	Tyr	His	Pro	Ser	Arg	Leu	Leu	Trp	Leu	Lys	Thr	Glu	Phe	Glu	Lys	
				150					155					160		
gag	ttc	aac	aaa	gcc	aag	tat	gtg	atg	acc	atc	ggg	gag	tac	gtc	tac	643
Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	Met	Thr	Ile	Gly	Glu	Tyr	Val	Tyr	
				170					175					180		
ttc	aaa	ctt	gca	ggc	atc	acc	gga	atg	gct	act	tcg	att	gcc	gcg	tgg	691
Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	Met	Ala	Thr	Ser	Ile	Ala	Ala	Trp	
				185					190					195		
agt	ggc	att	ttg	gac	gcc	cat	acc	ggc	gaa	ctt	gat	ctg	act	atc	ttg	739
Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	Gly	Glu	Leu	Asp	Leu	Thr	Ile	Leu	
				200					205					210		
gag	cac	atc	ggg	gtt	gat	ccg	gct	ctg	ttc	ggg	gag	atc	aga	aac	cct	787
Glu	His	Ile	Gly	Val	Asp	Pro	Ala	Leu	Phe	Gly	Glu	Ile	Arg	Asn	Pro	
				215					220					225		
gat	gaa	cca	gcc	acc	gat	gcc	aaa	gtt	gtc	gac	aaa	aag	tgg	aag	cac	835
Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	Val	Val	Asp	Lys	Lys	Trp	Lys	His	
				230					235					240		
														245		

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
250 255 260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
280 285 290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc	1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
295 300 305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa	1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
330 335 340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc	1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu	
375 380 385	
gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
390 395 400 405	
gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
410 415 420	
gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt	1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
440 445 450	
gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg	1507
Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtgggaacg 1602

Phe Asp Ala Leu Tyr Leu Lys Leu Val

490

cgc

1605

<210> 320

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
1 5 10 15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
145 150 155 160

Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
165 170 175

Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
180 185 190

Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
195 200 205

Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
210 215 220

Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
225 230 235 240

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
245 250 255

Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr
 260 265 270
 Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro
 275 280 285
 Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser
 290 295 300
 Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala
 305 310 315 320
 Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu
 325 330 335
 Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe
 340 345 350
 Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr
 355 360 365
 Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly
 370 375 380
 Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met
 385 390 395 400
 Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val
 405 410 415
 Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp
 420 425 430
 Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr
 435 440 445
 Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr
 450 455 460
 Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser
 465 470 475 480
 Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 485 490

<210> 321

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> FRXA01049

<400> 321

cacagtatgt ggagcagctg cgcgcggaaa tcgatgagaa ggcctaccac ggccgcaccg 60

 gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115
 Val Val Lys Thr Glu

															1	5	
ttc	gag	aaa	gag	ttc	aac	aaa	gcc	aag	tat	gtg	atg	acc	atc	ggt	gag	163	
Phe	Glu	Lys	Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	Met	Thr	Ile	Gly	Glu		
				10					15					20			
tac	gtc	tac	ttc	aaa	ctt	gca	ggc	atc	acc	gga	atg	gct	act	tcg	att	211	
Tyr	Val	Tyr	Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	Met	Ala	Thr	Ser	Ile		
				25					30					35			
gcc	gcg	tgg	agt	ggc	att	ttg	gac	gcc	cat	acc	ggc	gaa	ctt	gat	ctg	259	
Ala	Ala	Trp	Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	Gly	Glu	Leu	Asp	Leu		
				40					45					50			
act	atc	ttg	gag	cac	atc	ggg	gtt	gat	ccg	gct	ctg	ttc	ggg	gag	atc	307	
Thr	Ile	Leu	Glu	His	Ile	Gly	Val	Asp	Pro	Ala	Leu	Phe	Gly	Glu	Ile		
				55					60					65			
aga	aac	cct	gat	gaa	cca	gcc	acc	gat	gcc	aaa	gtt	gtc	gac	aaa	aag	355	
Arg	Asn	Pro	Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	Val	Val	Asp	Lys	Lys		
				70					75					80			
tgg	aag	cac	ctg	gaa	gaa	atc	cct	tgg	ttc	cat	gcc	att	cca	gac	ggc	403	
Trp	Lys	His	Leu	Glu	Glu	Ile	Pro	Trp	Phe	His	Ala	Ile	Pro	Asp	Gly		
				90					95					100			
tgg	cct	tcc	aac	att	ggc	cca	ggc	gcc	gtg	gat	tct	aaa	acc	gtc	gca	451	
Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp	Ser	Lys	Thr	Val	Ala		
				105					110					115			
gtc	gcc	gcc	gct	aca	tcc	ggc	gcc	atg	cgc	gtg	atc	ctt	ccg	agc	gtt	499	
Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro	Ser	Val		
				120					125					130			
ccc	gaa	cag	atc	ccc	tct	ggc	ctg	tgg	tgt	tac	cgc	gtt	tcc	cgc	gac	547	
Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser	Arg	Asp		
				135					140					145			
cag	tgc	atc	gtt	ggg	ggc	gca	ctc	aac	gac	gtc	gga	cgc	gcc	gtc	acc	595	
Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala	Val	Thr		
				150					155					160			
tgg	ctg	gaa	cgc	acc	att	atc	aag	cct	gaa	aac	ctc	gac	gaa	gtg	ctg	643	
Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu	Val	Leu		
				170					175					180			
atc	cgc	gaa	ccc	ctc	gaa	ggc	acc	cca	gct	gtc	ctg	ccg	ttc	ttc	tcc	691	
Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe	Phe	Ser		
				185					190					195			
ggg	gaa	cgc	tcc	atc	ggc	tgg	gca	gcc	tca	gcg	cag	gcc	acg	atc	acc	739	
Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr	Ile	Thr		
				200					205					210			
aac	att	cag	gaa	caa	acc	ggc	cct	gaa	cac	ttg	tgg	cgc	ggc	gtt	ttc	787	
Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly	Val	Phe		
				215					220					225			
gaa	gcc	ctc	gca	ctc	tcc	tac	cag	cgc	gtt	tgg	gaa	cac	atg	ggg	aaa	835	
Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met	Gly	Lys		
				230					235					240			
														245			

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883
 Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
 250 255 260

 gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931
 Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
 265 270 275

 gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt 979
 Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
 280 285 290

 atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca 1027
 Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
 295 300 305

 ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075
 Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
 310 315 320 325

 aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121
 Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 330 335

 cagtggaaacg cgc 1134

<210> 322

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Val Val Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val
 1 5 10 15

Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly
 20 25 30

Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr
 35 40 45

Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
 50 55 60

Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
 65 70 75 80

Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
 85 90 95

Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
 100 105 110

Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val
 115 120 125

Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
 130 135 140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
 145 150 155 160
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
 165 170 175
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
 180 185 190
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
 195 200 205
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
 210 215 220
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
 225 230 235 240
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
 245 250 255
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
 260 265 270
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
 275 280 285
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
 290 295 300
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
 305 310 315 320
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
 325 330 335

Val

<210> 323
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> FRXA01050

<400> 323
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60

aagaatatcc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro
 1 5

aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
 10 15 20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35

ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50

acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65

atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85

atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100

tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
 105 110 115

tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
 120 125 130

atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145

tcc tac cac cca tcg cgc ttg ctg tgg tgaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155

gag 597

<210> 324

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
 1 5 10 15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

				85						90					95
Ser	Phe	Ala	Ser	Ser	Leu	Ile	Leu	Val	Asp	Gly	Glu	Gly	Asn	Ala	Leu
			100					105					110		
Thr	Pro	Cys	Ile	Thr	Tyr	Ala	Asp	Ser	Arg	Ser	Ala	Gln	Tyr	Val	Glu
		115					120					125			
Gln	Leu	Arg	Ala	Glu	Ile	Asp	Glu	Lys	Ala	Tyr	His	Gly	Arg	Thr	Gly
	130					135					140				
Val	Cys	Leu	His	Thr	Ser	Tyr	His	Pro	Ser	Arg	Leu	Leu	Trp		
145					150					155					

<210> 325

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00202

<400> 325

ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc	tctaagtaat	tcttgaaagg	aaattttcac	atg	tac	gct	cgt	aaa	115
				Met	Tyr	Ala	Arg	Lys	
				1				5	

ctt	att	gct	ctg	tcc	gct	tct	gtc	gtt	ttg	gct	ttc	agc	ttg	tct	gct	163
Leu	Ile	Ala	Leu	Ser	Ala	Ser	Val	Val	Leu	Ala	Phe	Ser	Leu	Ser	Ala	
			10					15					20			

tgc	aac	cgt	gaa	tct	tct	ggc	acc	agc	gca	gac	ggc	ggc	tct	gcg	gat	211
Cys	Asn	Arg	Glu	Ser	Ser	Gly	Thr	Ser	Ala	Asp	Gly	Gly	Ser	Ala	Asp	
		25					30						35			

ggg	tcg	atc	acc	ttg	gct	ctg	tct	acc	cag	acc	aac	ccg	ttc	ttt	gtg	259
Gly	Ser	Ile	Thr	Leu	Ala	Leu	Ser	Thr	Gln	Thr	Asn	Pro	Phe	Phe	Val	
		40				45					50					

cag	ctt	cgt	gat	ggc	gcc	cag	gaa	aag	gct	gat	gaa	ttg	ggc	gtg	acc	307
Gln	Leu	Arg	Asp	Gly	Ala	Gln	Glu	Lys	Ala	Asp	Glu	Leu	Gly	Val	Thr	
	55				60					65						

ctc	aat	gtt	cag	gat	gct	tcc	gat	gac	gct	gca	acg	cag	gcc	aac	cag	355
Leu	Asn	Val	Gln	Asp	Ala	Ser	Asp	Asp	Ala	Ala	Thr	Gln	Ala	Asn	Gln	
	70				75				80					85		

ctc	aac	aac	gct	gtc	acc	acc	ggc	gct	ggc	gtg	gtg	att	gtc	aac	cca	403
Leu	Asn	Asn	Ala	Val	Thr	Thr	Gly	Ala	Gly	Val	Val	Ile	Val	Asn	Pro	
			90				95							100		

act	gat	tct	gat	gct	gtg	gtg	ccg	tcg	gtg	gaa	gct	ctc	aac	cag	gct	451
Thr	Asp	Ser	Asp	Ala	Val	Val	Pro	Ser	Val	Glu	Ala	Leu	Asn	Gln	Ala	
			105				110						115			

gac	att	cct	gtt	gtg	gct	gtc	gac	cgt	tcc	tcc	aat	ggc	gag	gtg	499
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp	Ile	Pro	Val	Val	Ala	Val	Asp	Arg	Ser	Ser	Asn	Gly	Gly	Glu	Val		
	120						125					130					
gcg	tcc	ttc	gtg	gca	tct	gac	aac	gtt	gct	ggc	ggc	gcg	cag	gct	gct	547	
Ala	Ser	Phe	Val	Ala	Ser	Asp	Asn	Val	Ala	Gly	Gly	Ala	Gln	Ala	Ala		
	135					140				145							
gca	gcc	ctg	gca	gag	gcg	atc	ggg	ggc	gaa	ggg	gaa	atc	ctc	atg	ctg	595	
Ala	Ala	Leu	Ala	Glu	Ala	Ile	Gly	Gly	Glu	Gly	Glu	Ile	Leu	Met	Leu		
	150				155				160						165		
caa	ggc	att	gcg	gga	tcc	tct	gca	tca	cgt	gat	cgt	gga	cag	gga	ttt	643	
Gln	Gly	Ile	Ala	Gly	Ser	Ser	Ala	Ser	Arg	Asp	Arg	Gly	Gln	Gly	Phe		
			170					175						180			
gaa	gag	gag	atc	gct	aag	cat	gag	ggc	att	tcc	att	gtg	gct	aag	cag	691	
Glu	Glu	Glu	Ile	Ala	Lys	His	Glu	Gly	Ile	Ser	Ile	Val	Ala	Lys	Gln		
			185				190					195					
acc	gcc	aac	ttt	gac	cgc	ggg	gag	ggc	ctg	gac	gtg	gca	act	aac	ctg	739	
Thr	Ala	Asn	Phe	Asp	Arg	Gly	Glu	Gly	Leu	Asp	Val	Ala	Thr	Asn	Leu		
	200					205					210						
ctg	cag	gca	cac	ccc	aat	gtg	aag	gcg	atc	ttc	gcg	gaa	aac	gat	gag	787	
Leu	Gln	Ala	His	Pro	Asn	Val	Lys	Ala	Ile	Phe	Ala	Glu	Asn	Asp	Glu		
	215				220					225							
atg	gcg	ttg	ggc	gca	atc	gaa	gcc	ctg	ggg	gct	cgt	gct	ggg	gaa	gat	835	
Met	Ala	Leu	Gly	Ala	Ile	Glu	Ala	Leu	Gly	Ala	Arg	Ala	Gly	Glu	Asp		
	230				235				240					245			
gtc	atc	gtt	gtc	ggg	ttc	gat	ggc	acc	aat	gat	ggg	ctg	gca	gcg	gtt	883	
Val	Ile	Val	Val	Gly	Phe	Asp	Gly	Thr	Asn	Asp	Gly	Leu	Ala	Ala	Val		
				250				255					260				
gaa	gat	gga	cgc	atg	ttg	gcc	acc	gtt	gct	cag	cag	cca	gaa	gag	ctg	931	
Glu	Asp	Gly	Arg	Met	Leu	Ala	Thr	Val	Ala	Gln	Gln	Pro	Glu	Glu	Leu		
			265				270					275					
gga	gca	aag	gct	gtg	gaa	gaa	gca	gct	aag	ctc	ctg	cgc	ggg	gag	gac	979	
Gly	Ala	Lys	Ala	Val	Glu	Glu	Ala	Ala	Lys	Leu	Leu	Arg	Gly	Glu	Asp		
	280					285				290							
gct	gaa	aca	gag	gta	cca	gtt	gag	gtt	gtc	act	gtg	aag	ctc	gac	aac	1027	
Ala	Glu	Thr	Glu	Val	Pro	Val	Glu	Val	Val	Thr	Val	Lys	Leu	Asp	Asn		
	295				300				305								
gtc	gcg	gac	ttc	aag	tagtcggcga	tgaaaaagtc	cgt									1065	
Val	Ala	Asp	Phe	Lys													
	310																

<210> 326

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala

1

5

10

15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30
 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 327
 <211> 1077
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1054)

<223> RXN00872

<400> 327

gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatc gtgagggtcg 60

ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115
 Met Thr Asn Leu Thr
 1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
 10 15 20

cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211
 Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
 25 30 35

tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259
 Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Arg His
 40 45 50

gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307
 Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
 55 60 65

gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355
 Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
 70 75 80 85

gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
 Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
 90 95 100

ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct 451
 Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
 105 110 115

ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499
 Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
 120 125 130

gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547
 Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
 135 140 145

agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc 595
 Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
 150 155 160 165

cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
 His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
 170 175 180

gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg 691
 Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
 185 190 195

gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag 739
Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr Glu
200 205 210

cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc 787
Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala
215 220 225

atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa 835
Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu
230 235 240 245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt 883
Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly
250 255 260

gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa 931
Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu
265 270 275

tgg cgc ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt 979
Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu
280 285 290

gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag 1027
Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu
295 300 305

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074
Val Glu Ala Ser Leu Asn Gln Lys Val
310 315

tct 1077

<210> 328
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 328
Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
1 5 10 15
Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
20 25 30
Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
35 40 45
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
50 55 60
Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
65 70 75 80
Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
85 90 95
Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

100					105					110						
Arg	Glu	Pro	Lys	Ala	Pro	Asp	Leu	Asn	Ile	Glu	Ser	Ala	Asp	Val	Ser	
115					120					125						
Leu	Asp	Asp	Val	Arg	Glu	Ala	Asp	Ile	Leu	Trp	Phe	Thr	Leu	Thr	Gly	
130					135					140						
Phe	Ser	Glu	Glu	Pro	Ser	Arg	Gly	Thr	His	Arg	Glu	Ile	Leu	Thr	Thr	
145					150					155					160	
Arg	Ala	Asn	Arg	Arg	His	Thr	Ile	Phe	Asp	Leu	Asp	Tyr	Arg	Pro	Met	
165					170					175						
Phe	Trp	Glu	Ser	Pro	Glu	Glu	Ala	Thr	Lys	Gln	Ala	Glu	Trp	Ala	Leu	
180					185					190						
Gln	His	Ser	Thr	Val	Ala	Val	Gly	Asn	Lys	Glu	Glu	Cys	Glu	Ile	Ala	
195					200					205						
Val	Gly	Glu	Thr	Glu	Pro	Glu	Arg	Ala	Gly	Arg	Ala	Leu	Leu	Glu	Arg	
210					215					220						
Gly	Val	Glu	Leu	Ala	Ile	Val	Lys	Gln	Gly	Pro	Lys	Gly	Val	Met	Ala	
225					230					235					240	
Met	Thr	Lys	Asp	Glu	Thr	Val	Glu	Val	Pro	Pro	Phe	Phe	Val	Asp	Val	
245					250					255						
Ile	Asn	Gly	Leu	Gly	Ala	Gly	Asp	Ala	Phe	Gly	Gly	Ala	Leu	Cys	His	
260					265					270						
Gly	Leu	Leu	Ser	Glu	Trp	Pro	Leu	Glu	Lys	Val	Leu	Arg	Phe	Ala	Asn	
275					280					285						
Thr	Ala	Gly	Ala	Leu	Val	Ala	Ser	Arg	Leu	Glu	Cys	Ser	Thr	Ala	Met	
290					295					300						
Pro	Thr	Thr	Asp	Glu	Val	Glu	Ala	Ser	Leu	Asn	Gln	Lys	Val			
305					310					315						

<210> 329
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622)
 <223> FRXA00872

<400> 329
 gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatc gtgaggggtcg 60

ccacattcca tcaaaaatga gtgaagggtt gcatgccac atg act aac ttg acg 115
 Met Thr Asn Leu Thr
 1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

	10	15	20	
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag				211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys				
	25	30	35	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat				259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Arg His				
	40	45	50	
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc				307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly				
	55	60	65	
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac				355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr				
	70	75	80	85
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att				403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile				
	90	95	100	
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct				451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala				
	105	110	115	
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc				499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg				
	120	125	130	
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca				547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro				
	135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc				595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg				
	150	155	160	165
cac acc atc ttt gat ctg gac tac cga				622
His Thr Ile Phe Asp Leu Asp Tyr Arg				
	170			

<210> 330

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
1 5 10 15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
20 25 30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
50 55 60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
 100 105 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
 145 150 155 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg
 165 170

<210> 331
 <211> 1767
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1744)
 <223> RXN00799

<400> 331
 ttgtctaacc ccgtataggt gagaaatggt ggacaagtgt ctgttttttg tgggggaaat 60

ctgactacga tggaagaaa taaggaaaga gattaccatt atg tct caa gag cgg 115
 Met Ser Gln Glu Arg
 1 5

cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163
 Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
 10 15 20

caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211
 Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
 25 30 35

tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259
 Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
 40 45 50

aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307
 Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
 55 60 65

gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355
 Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
 70 75 80 85

tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403
 Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro

90								95								100	
atc	acg	ggg	gtt	cct	ttc	acc	gag	cct	gtg	ctg	gca	act	tct	tcc	act	451	
Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser	Thr		
105								110								115	
gaa	aat	gcc	att	aac	ctg	cgc	aat	cag	cgt	tac	tta	att	gtt	cgt	gac	499	
Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg	Asp		
120								125								130	
aac	ctg	cca	gct	cgt	ggg	ctt	gct	act	tgg	acc	aat	gct	gtt	cag	gaa	547	
Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln	Glu		
135								140								145	
gtc	gcg	gag	cga	tcc	cgt	ttg	ggg	att	cct	gtt	gcg	ttt	gcg	tcg	aat	595	
Val	Ala	Glu	Arg	Ser	Arg	Leu	Gly	Ile	Pro	Val	Ala	Phe	Ala	Ser	Asn		
150								155								160	
cct	cgt	aac	cac	gtc	gcg	ctc	gtt	gcg	cag	ttc	ggg	gtg	aac	gag	tcc	643	
Pro	Arg	Asn	His	Val	Ala	Leu	Val	Ala	Gln	Phe	Gly	Val	Asn	Glu	Ser		
170								175								180	
gcg	ggg	gtg	ttc	tct	gag	tgg	cct	ggc	gag	ctg	ggg	ctt	gct	gcg	ctt	691	
Ala	Gly	Val	Phe	Ser	Glu	Trp	Pro	Gly	Glu	Leu	Gly	Leu	Ala	Ala	Leu		
185								190								195	
gcg	gat	gct	gaa	ctg	atg	gag	act	ttc	ggg	acc	gag	gct	gct	aaa	gaa	739	
Arg	Asp	Ala	Glu	Leu	Met	Glu	Thr	Phe	Gly	Thr	Glu	Ala	Ala	Lys	Glu		
200								205								210	
tgg	cgt	gcc	ggg	ggg	gtg	cac	aag	ctg	tac	ggg	tac	atg	gct	gac	ctc	787	
Trp	Arg	Ala	Gly	Gly	Val	His	Lys	Leu	Tyr	Gly	Tyr	Met	Ala	Asp	Leu		
215								220								225	
gct	tct	gag	cct	cgt	tgg	tcc	cgc	ttc	aac	ggg	act	ttt	ggg	gag	gat	835	
Ala	Ser	Glu	Pro	Arg	Trp	Ser	Arg	Phe	Asn	Gly	Thr	Phe	Gly	Glu	Asp		
230								235								240	
ccg	gag	ttg	atc	tct	gat	tac	atc	gct	gct	gtt	gtg	cgt	ggg	ttg	cag	883	
Pro	Glu	Leu	Ile	Ser	Asp	Tyr	Ile	Ala	Ala	Val	Val	Arg	Gly	Leu	Gln		
250								255								260	
ggc	cct	gag	ctg	tcc	aag	aat	tcc	gtg	tcg	acc	acc	att	aag	cac	ttc	931	
Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His	Phe		
265								270								275	
cca	ggg	ggc	ggc	gtg	cgc	ctc	gac	ggc	cac	gat	cct	cac	ttc	cac	tgg	979	
Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	Trp		
280								285								290	
ggg	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	cat	1027	
Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	His		
295								300								305	
ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	atg	1075	
Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	Met		
310								315								320	
cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	cag	1123	
Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	Gln		
330								335								340	

cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt gcc 1171
 Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala
 345 350 355
 tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc cac 1219
 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
 360 365 370
 cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg 1267
 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
 375 380 385
 ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg cgt 1315
 Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg
 390 395 400 405
 gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc 1363
 Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu
 410 415 420
 gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca 1411
 Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro
 425 430 435
 gtc cag cga ctc ctg gag gaa atc ttc cag ctt ggt ctg ttt gag aac 1459
 Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn
 440 445 450
 cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
 455 460 465
 gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg 1555
 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
 470 475 480 485
 cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
 490 495 500
 gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
 505 510 515
 aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
 520 525 530
 gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744
 Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
 535 540 545
 tgaaattgca ctgtttgaag atg 1767

<210> 332

<211> 548

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Met Ser Gln Glu Arg Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile
 1 5 10 15
 Glu Gln Asp Gly Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu
 20 25 30
 Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp
 35 40 45
 Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
 50 55 60
 Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
 65 70 75 80
 Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
 85 90 95
 Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
 100 105 110
 Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
 115 120 125
 Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
 130 135 140
 Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
 145 150 155 160
 Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
 165 170 175
 Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
 180 185 190
 Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
 195 200 205
 Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
 210 215 220
 Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
 225 230 235 240
 Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
 245 250 255
 Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
 260 265 270
 Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
 275 280 285
 Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
 290 295 300
 Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
 305 310 315 320

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala
 325 330 335
 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu
 340 345 350
 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg
 355 360 365
 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
 370 375 380
 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
 385 390 395 400
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn
 405 410 415
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
 420 425 430
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
 435 440 445
 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
 450 455 460
 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp
 465 470 475 480
 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser
 485 490 495
 Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp
 500 505 510
 Arg Arg Gly Ser Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro
 515 520 525
 Arg Gly Asn Leu Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg
 530 535 540
 Val Gly Ser Pro
 545

<210> 333

<211> 1607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1584)

<223> FRXA00799

<400> 333

cta caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa 48
 Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu
 1 5 10 15

gat tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt	96
Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg	
20 25 30	
atg aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac	144
Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr	
35 40 45	
ccc gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa	192
Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu	
50 55 60	
aag tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac	240
Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn	
65 70 75 80	
ccg atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc	288
Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser	
85 90 95	
act gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt	336
Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg	
100 105 110	
gac aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag	384
Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln	
115 120 125	
gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg	432
Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser	
130 135 140	
aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag	480
Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu	
145 150 155 160	
tcc gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg	528
Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala	
165 170 175	
ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa	576
Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys	
180 185 190	
gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac	624
Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp	
195 200 205	
ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag	672
Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu	
210 215 220	
gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg	720
Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu	
225 230 235 240	
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac	768
Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His	
245 250 255	
ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac	816

Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	
			260					265					270			
tgg	ggt	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	864
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	
		275					280					285				
cat	ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	912
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	
	290					295					300					
atg	cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	960
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	
305					310					315					320	
cag	cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	gtt	gcg	ttt	1008
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe	
				325					330					335		
gcc	tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	1056
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly	
			340					345					350			
cac	cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	1104
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met	
		355					360					365				
tgg	ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	1152
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val	
	370					375					380					
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu	
385					390					395					400	
ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln	
				405					410					415		
cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	1296
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu	
			420					425					430			
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggt	gcg	cca	1344
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro	
		435					440					445				
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu	
	450					455					460					
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro	
465					470					475					480	
gaa	gat	cta	ccc	att	ggt	tac	tgg	ccg	tac	caa	gat	cga	cga	ggt	tca	1488
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser	
				485					490					495		
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggt	aac	ctt	1536
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu	

500					505					510						
ggt	gtc	ttc	cga	gtc	aga	agc	aga	tct	tgc	aat	cgt	gtg	ggc	tcg	ccc	1584
Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro	
		515					520					525				

tgaaattgca ctgtttgaag atg 1607

<210> 334
 <211> 528
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 334
 Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu
 1 5 10 15
 Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg
 20 25 30
 Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr
 35 40 45
 Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
 50 55 60
 Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
 65 70 75 80
 Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser
 85 90 95
 Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
 100 105 110
 Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
 115 120 125
 Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
 130 135 140
 Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu
 145 150 155 160
 Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
 165 170 175
 Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys
 180 185 190
 Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp
 195 200 205
 Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu
 210 215 220
 Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu
 225 230 235 240
 Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His

245							250							255													
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His												
			260					265					270														
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr												
		275					280					285															
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile												
	290					295					300																
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp												
305					310					315				320													
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe												
				325					330					335													
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly												
			340					345					350														
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met												
		355					360					365															
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val												
	370					375					380																
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu												
385					390					395					400												
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln												
				405					410					415													
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu												
			420					425					430														
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro												
		435					440					445															
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu												
	450					455					460																
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro												
465					470					475					480												
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp																				

```
<210> 335
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum
```

<220>

<221> CDS

<222> (101)..(1609)

<223> RXA00032

<400> 335

```

cacttgctga agacgcccac atcgaagacc ttgcagatgt aaacgcaaac gcctaactgt 60
ttttcgagct aaacccatcc ttgaaaggat cttttccacc atg aac acc cca ctc 115
          *                               Met Asn Thr Pro Leu
                               1                               5

cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
          10                               15                               20

cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
          25                               30                               35

ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
          40                               45                               50

gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
          55                               60                               65

ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa 355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln
          70                               75                               80                               85

gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat 403
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp
          90                               95                               100

caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac 451
Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp
          105                               110                               115

cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt 499
Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val
          120                               125                               130

tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa 547
Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu
          135                               140                               145

gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg 595
Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu
          150                               155                               160                               165

cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act 643
Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr
          170                               175                               180

gcc gca ttg att tcc cga aaa gaa tca gga tct acg cca ttt acc atc 691
Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser Thr Pro Phe Thr Ile
          185                               190                               195

```

atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
200 205 210	
ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	
aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac	1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His	
310 315 320 325	
cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc	1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu	
330 335 340	
ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca	1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro	
345 350 355	
ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc	1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly	
360 365 370	
aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc	1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser	
375 380 385	
gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca	1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala	
390 395 400 405	
gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg	1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala	
410 415 420	
cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt	1411
Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val	
425 430 435	
gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc	1459

Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500
 act gtc taaatccggtt gcgcgctagg gtt 1632
 Thr Val

<210> 336

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala
 1 5 10 15
 Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala
 20 25 30
 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
 165 170 175
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
 180 185 190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
 195 200 205
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
 210 215 220
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
 225 230 235 240
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
 245 250 255
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
 260 265 270
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
 275 280 285
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
 290 295 300
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
 305 310 315 320
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
 325 330 335
 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
 340 345 350
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
 355 360 365
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
 370 375 380
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
 385 390 395 400
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
 405 410 415
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
 420 425 430
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
 435 440 445
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
 450 455 460
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
 465 470 475 480
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
 485 490 495
 Leu Leu Thr Gln Val Thr Val
 500

```
<220>
<221> CDS
<222> (101)..(1075)
<223> RXA02528
```

477

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg 691
 Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala
 185 190 195

gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct 739
 Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser
 200 205 210

gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt 787
 Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu
 215 220 225

ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg 835
 Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met
 230 235 240 245

cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att 883
 Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile
 250 255 260

ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att 931
 Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile
 265 270 275

acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc 979
 Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg
 280 285 290

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075
 Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly
 310 315 320 325

tagaattgcc caaatgtcat caa 1098

<210> 338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val
 1 5 10 15

Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser
 20 25 30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
 225 230 235 240
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
 245 250 255
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
 260 265 270
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
 275 280 285
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
 290 295 300
 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
 305 310 315 320
 Ser Thr His Ser Gly
 325

<210> 339

<211> 1246

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXN00316

<400> 339

agcgcatgat cgatgcctgc gagtccgcag ggggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc	cgcggtcaa	aaaatgaaaa	aggagccgtc	atg	ggc	caa	tgc	acg	115
				Met	Gly	Gln	Cys	Thr	
				1				5	
gta	gcg	ctt	tac	cga	gag	cat	tcc	tat	163
Val	Ala	Leu	Tyr	Arg	Glu	His	Ser	Tyr	
				10				15	
									20
gga	acc	tggt	gca	gcc	gat	ggc	ggg	gga	211
Gly	Thr	Trp	Ala	Ala	Asp	Gly	Gly	Gly	
			25					30	
									35
cac	tac	atc	gat	ctt	ttg	tac	tggt	ctg	259
His	Tyr	Ile	Asp	Leu	Leu	Tyr	Trp	Leu	
			40				45		
									50
ttc	ggc	tac	acc	aac	tcc	ttc	aaa	cac	307
Phe	Gly	Tyr	Thr	Asn	Ser	Phe	Lys	His	
	55					60			
									65
gac	agc	gcc	gtt	gcc	act	gtg	cgt	ttt	355
Asp	Ser	Ala	Val	Ala	Thr	Val	Arg	Phe	
	70				75				
									80
									85
att	tca	gcc	acc	acc	gcc	gca	gag	cca	403
Ile	Ser	Ala	Thr	Thr	Ala	Ala	Glu	Pro	
				90				95	
									100
gtg	atg	gga	aca	aag	ggg	gcc	acc	atg	451
Val	Met	Gly	Thr	Lys	Gly	Ala	Thr	Met	
			105					110	
									115
ggg	acc	gac	ggc	agg	ctc	att	gtt	cgc	499
Gly	Thr	Asp	Gly	Arg	Leu	Ile	Val	Arg	
		120					125		
									130
aac	cac	ccc	att	cca	ccc	cgc	gga	tct	547
Asn	His	Pro	Ile	Pro	Pro	Arg	Gly	Ser	
	135					140			
									145
cat	cat	caa	cgg	tgc	ttt	gat	ccc	gta	595
His	His	Gln	Arg	Cys	Phe	Asp	Pro	Val	
150					155				
									160
									165
ctt	tat	cga	tgc	gct	caa	cga	agg	ccg	643
Leu	Tyr	Arg	Cys	Ala	Gln	Arg	Arg	Pro	
				170				175	
									180
cga	tgc	cac	cag	agc	tct	gaa	agt	tct	691
Arg	Cys	His	Gln	Ser	Ser	Glu	Ser	Pro	
			185					190	
									195
agc	cac	cca	cca	gcc	ggg	ctc	ttt	gat	739
Ser	His	Pro	Pro	Ala	Gly	Leu	Phe	Asp	
		200					205		
									210
tca	cgc	caa	atc	ggg	ctt	gca	cct	tta	787
Ser	Arg	Gln	Ile	Gly	Leu	Ala	Pro	Leu	
	215					220			
									225

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835
 Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly
 230 235 240 245

ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883
 Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
 250 255 260

cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931
 Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
 265 270 275

gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979
 Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
 280 285 290

acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027
 Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
 295 300 305

gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075
 Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
 310 315 320 325

acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123
 Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
 330 335 340

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
 345 350 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
 360 365 370

acc ttg cac atg gcc agg ttc gga gcc 1246
 Thr Leu His Met Ala Arg Phe Gly Ala
 375 380

<210> 340

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95

Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
 100 105 110

Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
 115 120 125

Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser
 130 135 140

Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
 145 150 155 160

Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
 165 170 175

Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
 180 185 190

Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
 195 200 205

Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
 210 215 220

Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
 225 230 235 240

Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
 245 250 255

Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
 260 265 270

Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
 275 280 285

Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
 290 295 300

Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
 305 310 315 320

Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
 325 330 335

Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
 340 345 350

Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
 355 360 365

Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
 370 375 380

<210> 341

<211> 412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> FRXA00309

<400> 341

```

agcgcacgat cgatgcctgc gagtccgcag gggccaact tggcgtgctc ttccagcgcc 60
gcttctggcc cgcggctcaa aaaatgaaaa aggagccgtc atg ggc caa tgc acg 115
                                         Met Gly Gln Cys Thr
                                         1           5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
          10                15                20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
          25                30                35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
          40                45                50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
          55                60                65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
          70                75                80                85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
          90                95                100

gtg atg gga 412
Val Met Gly

```

<210> 342

<211> 104

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

```

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
  1           5           10          15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
  20                25                30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
  35                40                45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
  50                55                60

```

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95

Gly Ala Gln Val Gln Val Met Gly
 100

<210> 343

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN00310

<400> 343

ttgcgggatt catcatcggc gcaatcgac tgtctgccgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545

Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc

558

<210> 344
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 344
 Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 345
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> FRXA00310

<400> 345
 ttgcgggatt catcatcggc gcaatcgcac tgtctgccgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163

Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130
 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145
 ccgagagcat tcc 558

<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15
 Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30
 Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45
 Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60
 Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80
 Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110
 Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125
 Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 347
 <211> 1342
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1342)
 <223> RXA00041

<400> 347

atgaagcagc agcatccaag ctggaaaacg ctgatcacta ccgtctcatg gagcaattaa 60
 agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115
 Met His Thr Glu Leu
 1 5
 tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163
 Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu
 10 15 20
 aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211
 Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr
 25 30 35
 tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259
 Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp
 40 45 50
 gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307
 Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr
 55 60 65
 cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
 His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
 70 75 80 85
 tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403
 Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe
 90 95 100
 tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451
 Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn
 105 110 115
 ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc 499
 Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg

120					125					130						
cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggg	ttc	aca	547
Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	Thr	
135					140					145						
ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggg	gat	ggg	tgg	aaa	595
Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	Lys	
150					155					160					165	
atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggg	gca	gcg	gtt	cta	643
Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	Leu	
170					175					180						
tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggg	gaa	atc	acc	691
Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	Thr	
185					190					195						
ttt	gac	ctc	agt	gat	gca	caa	cct	ggg	tct	gct	cct	gat	ctc	gtt	ccc	739
Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	Pro	Asp	Leu	Val	Pro	
200					205					210						
ggg	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	ctt	ttt	acg	ctt	cgc	gat	gaa	787
Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	Thr	Leu	Arg	Asp	Glu	
215					220					225						
gaa	act	ggc	gaa	gat	ctc	gac	gtg	ctg	att	ttc	tgt	cca	caa	gga	ttg	835
Glu	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	Cys	Pro	Gln	Gly	Leu	
230					235					240					245	
gac	cga	atc	cac	gat	gag	gtt	act	cac	tac	gca	agc	tct	gac	cag	tgc	883
Asp	Arg	Ile	His	Asp	Glu	Val	Thr	His	Tyr	Ala	Ser	Ser	Asp	Gln	Cys	
250					255					260						
gga	tat	gtc	gtc	ggc	aag	ctt	gaa	gga	acg	acc	ttc	cgc	gtc	ttg	cga	931
Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Gly	Thr	Thr	Phe	Arg	Val	Leu	Arg	
265					270					275						
gga	ttc	agc	gag	ctg	gat	ttc	ggc	cat	gaa	ttc	tac	gca	ccg	cag	gtt	979
Gly	Phe	Ser	Glu	Leu	Asp	Phe	Gly	His	Glu	Phe	Tyr	Ala	Pro	Gln	Val	
280					285					290						
gca	gta	aac	ggg	tct	gat	gcc	tgg	ctc	gtg	ggc	tgg	atg	ggg	ctg	ccc	1027
Ala	Val	Asn	Gly	Ser	Asp	Ala	Trp	Leu	Val	Gly	Trp	Met	Gly	Leu	Pro	
295					300					305						
gcg	cag	gat	gat	cac	cca	aca	gtt	gca	cgg	gaa	gga	tgg	gtg	cac	tgc	1075
Ala	Gln	Asp	Asp	His	Pro	Thr	Val	Ala	Arg	Glu	Gly	Trp	Val	His	Cys	
310					315					320					325	
ctg	act	gtg	ccc	cgc	aag	ctt	cat	ttg	cgc	aac	cac	gcg	atc	tat	caa	1123
Leu	Thr	Val	Pro	Arg	Lys	Leu	His	Leu	Arg	Asn	His	Ala	Ile	Tyr	Gln	
330					335					340						
gag	ctt	ctt	ctc	cca	gag	ggg	gag	tca	ggg	gta	atc	aga	tct	gta	tta	1171
Glu	Leu	Leu	Leu	Pro	Glu	Gly	Glu	Ser	Gly	Val	Ile	Arg	Ser	Val	Leu	
345					350					355						
ggg	tct	gaa	cct	gtc	cga	gta	gac	atc	cga	ggc	aat	att	tcc	ctc	gag	1219
Gly	Ser	Glu	Pro	Val	Arg	Val	Asp	Ile	Arg	Gly	Asn	Ile	Ser	Leu	Glu	
360					365					370						

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
 375 380 385

gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
 390 395 400 405

att gag ata act gca ggt gat gga cag 1342
 Ile Glu Ile Thr Ala Gly Asp Gly Gln
 410

<210> 348

<211> 414

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 1 5 10 15

Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205

Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

<210> 349

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> RXA02026

<400> 349

cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48
 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 351
 <211> 1617
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1594)
 <223> RXA02061

<400> 351
 taacctgcct tcacctggga ttatccaccc atgtgtgatg aaatcgctac cctgaatcaa 60
 agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115
 Met Thr Asn Val Ser
 1 5
 ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163

Gly	Tyr	His	Arg	Pro	Glu	Leu	His	Ile	Thr	Ala	Glu	Ser	Gly	Val	Leu	
				10					15					20		
ttt	gca	cct	gca	ggc	gtt	ctg	ttg	gat	gac	gac	acg	tgg	cat	ttc	ttc	211
Phe	Ala	Pro	Ala	Gly	Val	Leu	Leu	Asp	Asp	Asp	Thr	Trp	His	Phe	Phe	
			25					30					35			
cac	cag	tac	cgt	ccc	tca	cca	gat	cac	ggc	ccc	agg	tgg	gcg	cac	caa	259
His	Gln	Tyr	Arg	Pro	Ser	Pro	Asp	His	Gly	Pro	Arg	Trp	Ala	His	Gln	
		40					45					50				
ttc	gca	gag	cgc	act	cca	ttt	gtg	tgg	gat	atc	tgc	gat	gac	gtg	cta	307
Phe	Ala	Glu	Arg	Thr	Pro	Phe	Val	Trp	Asp	Ile	Cys	Asp	Asp	Val	Leu	
	55					60					65					
gcc	cct	gaa	ggc	gat	gaa	acc	cag	gtt	cgc	gct	ggc	tca	gtg	gtg	tcc	355
Ala	Pro	Glu	Gly	Asp	Glu	Thr	Gln	Val	Arg	Ala	Gly	Ser	Val	Val	Ser	
70					75					80					85	
aac	aac	ggt	ggc	gtt	gat	ctg	tac	ttc	acc	tcg	gtt	gtt	ggc	ccc	act	403
Asn	Asn	Gly	Gly	Val	Asp	Leu	Tyr	Phe	Thr	Ser	Val	Val	Gly	Pro	Thr	
				90					95					100		
tcc	act	atc	cag	ttg	gca	cac	atc	aac	aac	atc	cgt	ggc	acc	acc	gaa	451
Ser	Thr	Ile	Gln	Leu	Ala	His	Ile	Asn	Asn	Ile	Arg	Gly	Thr	Thr	Glu	
			105					110					115			
ctg	atc	aat	gag	gac	gag	ctg	ggg	ctc	gat	cca	gat	gtc	tcc	cga	atc	499
Leu	Ile	Asn	Glu	Asp	Glu	Leu	Gly	Leu	Asp	Pro	Asp	Val	Ser	Arg	Ile	
		120					125					130				
ggc	gaa	gtg	gtt	ggc	aac	act	gat	ggt	tat	gta	aag	ttc	cgc	tca	ccg	547
Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro	
	135					140					145					
tgc	gtt	atc	cca	ggt	tgg	gaa	gac	caa	gga	aac	cgc	gat	gaa	ggc	cac	595
Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His	
150					155					160					165	
tca	gga	tgg	ttg	atg	ctc	gca	gtt	act	ggc	cca	gtt	gaa	gcc	cca	aca	643
Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr	
				170					175					180		
gta	gtg	gtc	ctc	gac	tcg	cca	gat	gga	aga	gaa	tgg	tcc	att	aca	ggt	691
Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly	
			185					190					195			
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta	739
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu	
		200					205					210				
gtt	gct	cct	cgc	atg	att	cgt	ctg	cgc	gat	gaa	gtg	gat	cat	gaa	atc	787
Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile	
	215					220					225					
tac	gat	gtc	ctc	att	gtc	acc	att	gaa	caa	gac	ggg	att	gac	att	tcg	835
Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser	
230					235					240					245	
gga	tac	ctg	gta	ggc	cag	ctc	aac	ggc	tca	gaa	ttc	gat	gtg	aag	act	883
Gly	Tyr	Leu	Val	Gly	Gln	Leu	Asn	Gly	Ser	Glu	Phe	Asp	Val	Lys	Thr	

250										255					260					
cca	ttt	acc	cgc	atc	gat	ttt	ggc	cat	gat	ttc	tct	cgc	ccc	cgc	aac	931				
Pro	Phe	Thr	Arg	Ile	Asp	Phe	Gly	His	Asp	Phe	Ser	Arg	Pro	Arg	Asn					
			265					270					275							
acc	aac	tac	gcc	gaa	acc	acc	atc	ggc	tac	gac	ttc	gcc	cac	atc	ttt	979				
Thr	Asn	Tyr	Ala	Glu	Thr	Thr	Ile	Gly	Tyr	Asp	Phe	Ala	His	Ile	Phe					
			280					285					290							
ggt	ctc	atg	aat	ggc	gta	ggt	cgt	ttg	gac	tcc	ccc	act	gag	cat	ctc	1027				
Gly	Leu	Met	Asn	Gly	Val	Gly	Arg	Leu	Asp	Ser	Pro	Thr	Glu	His	Leu					
			295					300					305							
agt	tgg	aag	gaa	gaa	ggc	tgg	gca	aac	gct	att	tct	ttc	cca	cgt	att	1075				
Ser	Trp	Lys	Glu	Glu	Gly	Trp	Ala	Asn	Ala	Ile	Ser	Phe	Pro	Arg	Ile					
310						315					320					325				
gtc	acg	ctc	cag	gac	ggt	acg	gtc	ttc	cag	acc	cct	cca	gaa	gga	ttg	1123				
Val	Thr	Leu	Gln	Asp	Gly	Thr	Val	Phe	Gln	Thr	Pro	Pro	Glu	Gly	Leu					
			330					335					340							
ctt	gat	gcc	att	cat	gaa	tcc	gag	gca	gcg	gca	ggt	tgg	acc	gga	ctg	1171				
Leu	Asp	Ala	Ile	His	Glu	Ser	Glu	Ala	Ala	Ala	Gly	Trp	Thr	Gly	Leu					
			345					350					355							
tgc	gaa	atc	cca	tca	aac	agc	gca	gtt	gaa	gtg	gcg	ttg	aag	gac	caa	1219				
Cys	Glu	Ile	Pro	Ser	Asn	Ser	Ala	Val	Glu	Val	Ala	Leu	Lys	Asp	Gln					
			360					365					370							
gaa	ggt	gaa	atc	gct	gca	aca	atc	act	cac	cgc	cac	aat	cag	cta	gtc	1267				
Glu	Gly	Glu	Ile	Ala	Ala	Thr	Ile	Thr	His	Arg	His	Asn	Gln	Leu	Val					
			375					380					385							
gtt	gat	cgg	tcc	atg	aac	ccc	aac	cac	gcg	ggt	gat	cca	cac	gcg	att	1315				
Val	Asp	Arg	Ser	Met	Asn	Pro	Asn	His	Ala	Gly	Asp	Pro	His	Ala	Ile					
390						395					400					405				
gca	cca	ttg	act	gat	gat	gaa	aca	gat	tca	ctg	ttc	att	gtc	gtt	gac	1363				
Ala	Pro	Leu	Thr	Asp	Asp	Glu	Thr	Asp	Ser	Leu	Phe	Ile	Val	Val	Asp					
			410					415					420							
ggc	tct	aca	gta	gaa	gtt	ttt	gct	gat	ggc	ggt	tat	gta	tca	atg	gca	1411				
Gly	Ser	Thr	Val	Glu	Val	Phe	Ala	Asp	Gly	Gly	Tyr	Val	Ser	Met	Ala					
			425					430					435							
agc	cgt	gtg	tat	ttc	aac	aac	gga	cca	ttc	agc	gaa	ttt	gag	gtc	acc	1459				
Ser	Arg	Val	Tyr	Phe	Asn	Asn	Gly	Pro	Phe	Ser	Glu	Phe	Glu	Val	Thr					
			440					445					450							
acc	acc	ggt	gac	gca	agc	att	att	cgc	cag	gaa	agt	cac	ttc	cct	gtt	1507				
Thr	Thr	Gly	Asp	Ala	Ser	Ile	Ile	Arg	Gln	Glu	Ser	His	Phe	Pro	Val					
			455					460					465							
gat	ttc	agt	tcg	gtg	tcc	cta	gat	ata	gat	gat	ctc	act	gcg	ctc	atg	1555				
Asp	Phe	Ser	Ser	Val	Ser	Leu	Asp	Ile	Asp	Asp	Leu	Thr	Ala	Leu	Met					
470						475					480					485				
cag	ttc	gat	gaa	aac	gaa	ccg	cat	gaa	ggc	cca	gtg	aga	taagagttag			1604				
Gln	Phe	Asp	Glu	Asn	Glu	Pro	His	Glu	Gly	Pro	Val	Arg								
			490					495												

atgcgttcca gcc

1617

<210> 352

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala
 1 5 10 15

Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
 20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
 245 250 255

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
 260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp
 275 280 285
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser
 290 295 300
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile
 305 310 315 320
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr
 325 330 335
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala
 340 345 350
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val
 355 360 365
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg
 370 375 380
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly
 385 390 395 400
 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu
 405 410 415
 Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly
 420 425 430
 Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser
 435 440 445
 Glu Phe Glu Val Thr Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu
 450 455 460
 Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp
 465 470 475 480
 Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro
 485 490 495

Val Arg

<210> 353
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXN01369

<400> 353
 ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60
 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
 Met Glu Leu Leu Glu

															1	5	
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat	Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp	10	15	20	163												
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg	Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp	25	30	35	211												
ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc	Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu	40	45	50	259												
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt	Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val	55	60	65	307												
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca	Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala	70	75	80	355												
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc	Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala	90	95	100	403												
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca	Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala	105	110	115	451												
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt	Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val	120	125	130	499												
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac	Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn	135	140	145	547												
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac	Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr	150	155	160	595												
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg	Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu	170	175	180	643												
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc	Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile	185	190	195	691												
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt	Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg	200	205	210	739												
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa	Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu	215	220	225	787												
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc	Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe	230	235	240	835												

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt 883
 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
 250 255 260

cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
 265 270 275

aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
 280 285 290

ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
 295 300 305

gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
 310 315 320 325

ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
 330 335 340

gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
 345 350 355

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
 375 380 385

ttc ctc gct agg gtt tagatctttt tagattaaaa tca 1305
 Phe Leu Ala Arg Val
 390

<210> 354

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 354

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg
 1 5 10 15

Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
 20 25 30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu

65	70	75	80
Leu Lys Ile Leu	Ala Ala Gly Ala Pro	Leu Ser Leu Gln Ala His Pro	
	85	90	95
Ser Leu Glu Gln	Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly		
	100	105	110
Ile Asp Leu Gly	Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys		
	115	120	125
Pro Glu Leu Ile Val	Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe		
	130	135	140
Arg Pro Leu Arg Asn Thr	Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu		
	145	150	155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu			
	165	170	175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys			
	180	185	190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu			
	195	200	205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile			
	210	215	220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala			
	225	230	235
Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu			
	245	250	255
Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile			
	260	265	270
Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr			
	275	280	285
Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu			
	290	295	300
Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro			
	305	310	315
Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu			
	325	330	335
Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly			
	340	345	350
Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly			
	355	360	365
His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser			
	370	375	380
Glu Asp Ala Glu Val Phe Leu Ala Arg Val			
	385	390	

<210> 355
 <211> 524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(501)
 <223> FRXA01369

<400> 355
 aac gaa cag tgc ctc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg 48
 Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
 1 5 10 15

aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30

aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45

tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60

ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80

gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95

aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110

aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125

ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140

tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160

gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524
 Glu Val Phe Leu Ala Arg Val
 165

<210> 356
 <211> 167
 <212> PRT

<213> Corynebacterium glutamicum

<400> 356

```

Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
 1              5              10              15

Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
      20              25              30

Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
      35              40              45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
      50              55              60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
      65              70              75              80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
      85              90              95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
      100              105              110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
      115              120              125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
      130              135              140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
      145              150              155              160

Glu Val Phe Leu Ala Arg Val
      165

```

<210> 357

<211> 808

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> FRXA01373

<400> 357

```

ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60

gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
              Met Glu Leu Leu Glu
              1              5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
              10              15              20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
              25              30              35

```


ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259
 Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
 40 45 50
 aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt 307
 Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
 55 60 65
 gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355
 Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
 70 75 80 85
 gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc 403
 Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
 90 95 100
 cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451
 Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
 105 110 115
 ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt 499
 Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
 120 125 130
 gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547
 Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
 135 140 145
 acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595
 Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
 150 155 160 165
 cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643
 Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
 170 175 180
 ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691
 Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
 185 190 195
 gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739
 Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
 200 205 210
 gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787
 Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
 215 220 225
 cag tac ccc ggc gat gtc ggc 808
 Gln Tyr Pro Gly Asp Val Gly
 230 235

<210> 358

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg

1	5	10	15
Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro	20	25	30
Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile	35	40	45
Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala	50	55	60
Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu	65	70	75
Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro	85	90	95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly	100	105	110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys	115	120	125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe	130	135	140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu	145	150	155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu	165	170	175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys	180	185	190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu	195	200	205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile	210	215	220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly	225	230	235

<210> 359

<211> 1775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (1752)

<223> RXA02611

<400> 359

gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act	48
Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr	
1 5 10 15	

aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag	96
---	----

Lys	Ile	Glu	Ala	Gly	Gln	Gly	Ser	Asp	Glu	Leu	Tyr	Asn	Asp	Phe	Glu	
			20					25					30			
cac	ggg	gct	cag	ctg	ttt	gag	cgt	gct	gcg	gag	aat	ttg	tct	aaa	gag	144
His	Gly	Ala	Gln	Leu	Phe	Glu	Arg	Ala	Ala	Glu	Asn	Leu	Ser	Lys	Glu	
			35				40					45				
gat	agg	act	gcg	ctt	ttc	gac	gtc	gcc	tcc	tct	ctg	cgg	cgc	ggc	ggc	192
Asp	Arg	Thr	Ala	Leu	Phe	Asp	Val	Ala	Ser	Ser	Leu	Arg	Arg	Gly	Gly	
	50					55					60					
gat	gta	cgc	gca	cgt	ctc	gcc	cca	gcg	ctc	acc	gcg	agt	gtc	act	cat	240
Asp	Val	Arg	Ala	Arg	Leu	Ala	Pro	Ala	Leu	Thr	Ala	Ser	Val	Thr	His	
	65				70					75					80	
ctt	tta	gaa	ctt	aac	ccg	ttg	cgt	gag	ttg	gtc	acg	atg	ggg	gaa	aac	288
Leu	Leu	Glu	Leu	Asn	Pro	Leu	Arg	Glu	Leu	Val	Thr	Met	Gly	Glu	Asn	
				85				90						95		
ctg	cag	gtt	cgt	gtc	gag	cgt	cgt	gcc	gct	ttg	gtc	aac	tct	tgg	tat	336
Leu	Gln	Val	Arg	Val	Glu	Arg	Arg	Ala	Ala	Leu	Val	Asn	Ser	Trp	Tyr	
			100					105					110			
gag	ctt	ttc	cct	cgt	tcc	aca	ggg	ggg	tgg	gat	gag	tcc	ggc	acc	ccc	384
Glu	Leu	Phe	Pro	Arg	Ser	Thr	Gly	Gly	Trp	Asp	Glu	Ser	Gly	Thr	Pro	
		115					120					125				
gtt	cat	ggc	act	ttc	gct	acc	act	gct	cag	gcg	ttg	gag	cgt	gtc	gcg	432
Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala	
	130					135					140					
aag	atg	ggc	ttc	gat	act	gtt	tac	ttc	ccg	ccg	atc	cat	ccg	att	ggc	480
Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly	
	145				150				155						160	
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His	
				165				170						175		
gat	gtg	ggg	tcg	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggg	ggg	cat	gat	576
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp	
			180					185						190		
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu	
		195					200					205				
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu	
	210					215					220					
cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe	
	225				230				235					240		
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys	
				245				250						255		
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys	

260										265										270									
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggt	864													
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly														
		275					280					285																	
gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912													
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe														
		290				295					300																		
tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960													
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile														
		305			310					315					320														
ttc	cta	gcg	gag	gcg	tct	act	cgc	ccg	gca	cgt	ctg	tat	ttc	ttg	tcc	1008													
Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser														
				325					330					335															
aag	att	ggt	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056													
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr														
			340					345					350																
aac	gag	gag	ctc	acc	gag	ttc	gct	act	gag	atc	gcc	ccc	atg	gcg	gat	1104													
Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp														
		355					360					365																	
att	tct	cgt	ccg	aac	ctg	ttt	gtg	aac	act	ccc	gac	att	ttg	cat	gcg	1152													
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala														
		370				375					380																		
tct	ctg	cag	cat	ggt	gga	cgc	gcc	atg	ttc	gct	atc	cgc	gcc	gca	ttg	1200													
Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu														
		385			390					395					400														
gcc	gcc	acg	atg	tct	cct	gtg	tgg	ggc	gta	tat	tcc	gga	tat	gag	ctc	1248													
Ala	Ala	Thr	Met	Ser	Pro	Val	Trp	Gly	Val	Tyr	Ser	Gly	Tyr	Glu	Leu														
				405				410						415															
ttt	gag	cac	gag	gcc	gtc	aag	cct	ggt	tgc	gaa	gag	tac	ttg	gat	tct	1296													
Phe	Glu	His	Glu	Ala	Val	Lys	Pro	Gly	Ser	Glu	Glu	Tyr	Leu	Asp	Ser														
			420					425					430																
gag	aag	tac	gag	ctg	cgt	ccc	cgc	gat	ttc	gag	ggt	gct	ctg	gaa	cgt	1344													
Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg														
		435					440					445																	
ggc	gat	tct	ctc	gag	gat	tac	atc	gct	ctg	ctc	aac	cag	atc	cgt	cgc	1392													
Gly	Asp	Ser	Leu	Glu	Asp	Tyr	Ile	Ala	Leu	Leu	Asn	Gln	Ile	Arg	Arg														
		450				455					460																		
gcg	aac	cct	gcc	ttg	cag	caa	cta	cgc	aac	atc	cac	ttc	cac	gaa	gcg	1440													
Ala	Asn	Pro	Ala	Leu	Gln	Gln	Leu	Arg	Asn	Ile	His	Phe	His	Glu	Ala														
		465			470				475					480															
gac	aat	gat	cag	atc	atc	gcc	tac	tcc	aag	gtt	gat	gct	ttg	acc	gga	1488													
Asp	Asn	Asp	Gln	Ile	Ile	Ala	Tyr	Ser	Lys	Val	Asp	Ala	Leu	Thr	Gly														
			485					490					495																
aat	acc	gtg	ttg	att	gtg	gtc	aac	ttg	gat	cca	cgt	agt	gct	cgt	gag	1536													
Asn	Thr	Val	Leu	Ile	Val	Val	Asn	Leu	Asp	Pro	Arg	Ser	Ala	Arg	Glu														
		500					505						510																

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
 515 520 525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
 530 535 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
 545 550 555 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
 565 570 575

cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc 1775
 Arg Glu Ile Lys Thr Tyr Arg Ala
 580

<210> 360

<211> 584

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
 1 5 10 15

Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu
 20 25 30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
 35 40 45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
 50 55 60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65 70 75 80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
 85 90 95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
 100 105 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
 115 120 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
 130 135 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
 145 150 155 160

Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
 165 170 175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
 180 185 190
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
 195 200 205
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
 210 215 220
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
 225 230 235 240
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
 245 250 255
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
 260 265 270
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
 275 280 285
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
 290 295 300
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
 305 310 315 320
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
 325 330 335
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
 340 345 350
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
 355 360 365
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
 370 375 380
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
 385 390 395 400
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
 405 410 415
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
 420 425 430
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
 435 440 445
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
 450 455 460
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
 465 470 475 480
 Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly
 485 490 495
 Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu

500	505	510
Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala		
515	520	525
Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser		
530	535	540
Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile		
545	550	555
Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp		
565	570	575
Arg Glu Ile Lys Thr Tyr Arg Ala		
580		

<210> 361
 <211> 2316
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2293)
 <223> RXA02612

<400> 361
 gaacttccag cgtctcgccg tgagcgtctc gcgtggcgcg aaatcaagac ctaccgcgcg 60
 taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc 115
 Met Thr Val Asp Pro
 1 5
 gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163
 Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
 10 15 20
 tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211
 Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
 25 30 35
 gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat 259
 Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn
 40 45 50
 ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac 307
 Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
 55 60 65
 att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355
 Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
 70 75 80 85
 gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403
 Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr
 90 95 100
 tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451
 Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu

105						110						115						
gga	cgc	cat	gag	cgt	ttg	tgg	gag	att	ctc	ggt	gcc	aac	atc	aag	acc	499		
Gly	Arg	His	Glu	Arg	Leu	Trp	Glu	Ile	Leu	Gly	Ala	Asn	Ile	Lys	Thr			
		120					125					130						
tac	caa	act	gcg	ctc	gga	aca	gtt	cgt	ggc	acc	gca	ttt	act	gtg	tgg	547		
Tyr	Gln	Thr	Ala	Leu	Gly	Thr	Val	Arg	Gly	Thr	Ala	Phe	Thr	Val	Trp			
	135					140					145							
gct	cca	aac	gca	att	ggc	tgc	gca	gtg	gtc	ggt	ggc	ttc	aac	ggt	tgg	595		
Ala	Pro	Asn	Ala	Ile	Gly	Cys	Ala	Val	Val	Gly	Gly	Phe	Asn	Gly	Trp			
150					155					160					165			
aat	gca	tcc	cag	cat	ccg	atg	cgt	tct	atg	ggt	ggt	tcg	ggt	ctg	tgg	643		
Asn	Ala	Ser	Gln	His	Pro	Met	Arg	Ser	Met	Gly	Gly	Ser	Gly	Leu	Trp			
				170					175					180				
gag	ctg	ttc	atc	cca	ggc	ata	gag	gaa	ggc	gaa	gtg	tac	aaa	ttc	gcc	691		
Glu	Leu	Phe	Ile	Pro	Gly	Ile	Glu	Glu	Gly	Glu	Val	Tyr	Lys	Phe	Ala			
			185					190					195					
gtc	caa	acc	agg	gaa	ggc	caa	cgt	cgt	gat	aag	gcc	gat	ccg	atg	gct	739		
Val	Gln	Thr	Arg	Glu	Gly	Gln	Arg	Arg	Asp	Lys	Ala	Asp	Pro	Met	Ala			
		200					205					210						
cgt	cgc	gca	gaa	ctg	gcg	ccg	gca	acc	gga	tct	att	gtc	gct	tcc	tct	787		
Arg	Arg	Ala	Glu	Leu	Ala	Pro	Ala	Thr	Gly	Ser	Ile	Val	Ala	Ser	Ser			
	215					220					225							
gag	tac	cag	tgg	cag	gat	tcc	gag	tgg	ctg	cgc	gag	cgt	tcc	caa	act	835		
Glu	Tyr	Gln	Trp	Gln	Asp	Ser	Glu	Trp	Leu	Arg	Glu	Arg	Ser	Gln	Thr			
230					235					240					245			
gat	ctc	gca	tcc	aag	cca	atg	agt	gtc	tac	gag	gtc	cac	ctc	ggt	tct	883		
Asp	Leu	Ala	Ser	Lys	Pro	Met	Ser	Val	Tyr	Glu	Val	His	Leu	Gly	Ser			
				250					255					260				
tgg	cgc	tgg	ggt	aag	aac	tat	gag	gat	ttg	gct	act	gag	ctg	gtt	gat	931		
Trp	Arg	Trp	Gly	Lys	Asn	Tyr	Glu	Asp	Leu	Ala	Thr	Glu	Leu	Val	Asp			
			265					270						275				
tac	gtc	gca	gat	ctt	ggc	tac	acc	cac	gtg	gaa	ttc	ctc	cct	gtc	gca	979		
Tyr	Val	Ala	Asp	Leu	Gly	Tyr	Thr	His	Val	Glu	Phe	Leu	Pro	Val	Ala			
		280					285					290						
gag	cac	ccc	ttc	ggt	ggt	tcc	tgg	ggt	tac	cag	gtc	acc	ggc	tac	tac	1027		
Glu	His	Pro	Phe	Gly	Gly	Ser	Trp	Gly	Tyr	Gln	Val	Thr	Gly	Tyr	Tyr			
	295					300					305							
gca	ccg	acc	tct	cgt	tgg	ggt	act	cca	gat	cag	ttc	cgt	gcg	cta	gtc	1075		
Ala	Pro	Thr	Ser	Arg	Trp	Gly	Thr	Pro	Asp	Gln	Phe	Arg	Ala	Leu	Val			
310					315					320					325			
gac	gct	ttc	cac	gcc	cgc	ggt	att	ggc	gtg	atc	atg	gac	tgg	gtt	cct	1123		
Asp	Ala	Phe	His	Ala	Arg	Gly	Ile	Gly	Val	Ile	Met	Asp	Trp	Val	Pro			
				330					335					340				
gcc	cac	ttc	cct	aag	gat	gat	tgg	gct	ctt	gcc	cgc	ttt	gat	ggc	gaa	1171		
Ala	His	Phe	Pro	Lys	Asp	Asp	Trp	Ala	Leu	Ala	Arg	Phe	Asp	Gly	Glu			
			345					350					355					

gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg	1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
360 365 370	
ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc	1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
440 445 450	
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg	1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
570 575 580	
gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc 1939
 Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val
 600 605 610

tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc 1987
 Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly
 615 620 625

ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035
 Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe
 630 635 640 645

act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083
 Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu
 650 655 660

tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc 2131
 Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly
 665 670 675

gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca 2179
 Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala
 680 685 690

gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat 2227
 Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp
 695 700 705

aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
 710 715 720 725

ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316
 Phe Tyr Ser Leu Gln Lys
 730

<210> 362

<211> 731

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu
 1 5 10 15

Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
 20 25 30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
 35 40 45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
 50 55 60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65 70 75 80

Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
 85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
 100 105 110
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
 115 120 125
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
 130 135 140
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
 145 150 155 160
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
 165 170 175
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
 180 185 190
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
 195 200 205
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
 210 215 220
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
 225 230 235 240
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
 245 250 255
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
 260 265 270
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
 275 280 285
 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
 290 295 300
 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
 305 310 315 320
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
 325 330 335
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
 340 345 350
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
 355 360 365
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
 370 375 380
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
 385 390 395 400
 His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
 405 410 415
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly

420					425					430						
Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr	
435					440					445						
Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr	
450					455					460						
Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe	
465					470					475					480	
Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe	
485					490					495						
Ser	Lys	Asn	Pro	Val	His	Arg	Ala	Phe	His	His	Ser	Glu	Leu	Thr	Phe	
500					505					510						
Ser	Leu	Val	Tyr	Ala	Phe	Ser	Glu	Arg	Phe	Val	Leu	Pro	Ile	Ser	His	
515					520					525						
Asp	Glu	Val	Val	His	Gly	Lys	Gly	Ser	Leu	Trp	Asp	Arg	Met	Pro	Gly	
530					535					540						
Asp	Thr	Trp	Asn	Lys	Ala	Ala	Gly	Leu	Arg	Thr	Phe	Leu	Ala	Tyr	Met	
545					550					555					560	
Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly	
565					570					575						
Gln	Arg	Glu	Glu	Trp	Ala	Glu	Gly	Gln	Gly	Leu	Pro	Trp	Asp	Ile	Val	
580					585					590						
Asp	Gly	Trp	Gln	Gly	Glu	Tyr	His	Glu	Ala	Ile	Arg	Thr	Leu	Thr	Arg	
595					600					605						
Ser	Leu	Asn	Gly	Val	Tyr	Ser	Asp	Ser	Pro	Ala	Leu	His	Thr	Gln	Asp	
610					615					620						
Phe	Thr	Gly	Glu	Gly	Phe	Thr	Trp	Asn	Lys	Gly	Asp	Asp	Ala	Thr	Asn	
625					630					635					640	
Asn	Ile	Leu	Ala	Phe	Thr	Arg	Phe	Gly	Ser	Asp	Gly	Ser	Gln	Met	Leu	
645					650					655						
Cys	Val	Phe	Asn	Leu	Ser	Gly	Thr	Ser	Gln	Pro	Glu	Tyr	Gln	Leu	Gly	
660					665					670						
Val	Ala	Ala	Gly	Gly	Glu	Trp	Lys	Leu	Val	Leu	Asn	Thr	Asp	Asp	Ala	
675					680					685						
Glu	Phe	Leu	Gly	Ala	Glu	Asn	Asp	Ile	Ala	Thr	Ser	Val	Gln	Ala	Ala	
690					695					700						
Ala	Thr	Pro	Arg	Asp	Asn	Phe	Ala	Tyr	Ser	Leu	Ser	Leu	His	Val	Pro	
705					710					715					720	
Ala	Met	Ser	Ala	Gln	Phe	Tyr	Ser	Leu	Gln	Lys						
725					730											

<210> 363

<211> 1913
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1890)
 <223> RXN01884

<400> 363

gtg act gcc att gaa ttg atg ccg gtc cac cag ttc ctg cag gat gat	48
Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp	
1 5 10 15	
cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc	96
Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe	
20 25 30	
ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt	144
Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly	
35 40 45	
ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg	192
Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala	
50 55 60	
ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc	240
Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly	
65 70 75 80	
aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg	288
Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala	
85 90 95	
tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc	336
Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr	
100 105 110	
ggg act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg	384
Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu	
115 120 125	
att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc	432
Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly	
130 135 140	
ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt	480
Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val	
145 150 155 160	
gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc	528
Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val	
165 170 175	
tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga	576
Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly	
180 185 190	
tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa	624
Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys	
195 200 205	

tac	cgc	gac	act	gtc	cgt	gat	ttc	tgg	cgt	ggg	gag	cca	gca	acc	ttg	672
Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu	
210						215					220					
ggg	gaa	ttc	gct	tcc	cga	cta	act	ggg	tcc	tct	gat	ttg	tat	gca	aac	720
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn	
225					230				235						240	
aac	ggc	cgt	cgc	ccc	act	gca	tcg	atc	aac	ttt	gtg	act	gct	cac	gac	768
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp	
				245					250					255		
ggc	ttc	acc	ctc	aat	gac	ttg	gtc	agt	tac	aac	gag	aag	cac	aac	atg	816
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met	
			260					265					270			
gcc	aac	ggg	gaa	gac	ggg	cgg	gac	ggg	gaa	tca	cac	aac	cgt	tcc	tgg	864
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp	
		275				280						285				
aac	tgt	ggc	gtc	gaa	gga	cca	act	gac	gat	cct	gag	att	atg	cag	ctg	912
Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu	
290						295					300					
cgt	gct	cag	caa	cga	cgc	aac	ttc	ctc	acc	acc	ttg	ttg	ctg	tcc	cag	960
Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln	
305					310					315					320	
ggc	acc	cct	atg	ttg	tcc	cac	ggg	gat	gaa	atg	gcc	cgt	acc	caa	aac	1008
Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn	
				325					330					335		
ggc	aac	aac	aac	gtc	tac	tgc	caa	gac	aat	gaa	ctg	gcg	tgg	gtg	aat	1056
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn	
			340					345					350			
tgg	gat	cag	gct	gaa	gaa	aac	gct	gac	ttg	gtg	agc	ttc	acc	agg	cgt	1104
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg	
		355					360					365				
ttg	ctg	cgt	atc	cga	gca	aac	cac	cca	gta	ttt	agg	cgc	agg	cag	ttc	1152
Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	Arg	Arg	Arg	Gln	Phe	
		370				375					380					
ctt	gcc	ggg	ggc	cct	ttg	ggc	gcc	gat	gtt	cgt	gac	cgc	gat	atc	gca	1200
Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	Asp	Arg	Asp	Ile	Ala	
385					390					395					400	
tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	gat	gac	tgg	gac	ttc	1248
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe	
				405					410					415		
gct	ttc	ggg	aaa	tca	ctg	cag	gtg	ttc	ttc	aac	ggc	gat	gcc	atc	gaa	1296
Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	Gly	Asp	Ala	Ile	Glu	
			420					425					430			
gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	gac	tcc	ttc	atc	ttg	1344
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu	
		435					440					445				

atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag 1392
 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
 450 455 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg 1440
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
 465 470 475 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act 1488
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
 485 490 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac 1536
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
 500 505 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa 1584
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
 515 520 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg 1632
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
 530 535 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca 1680
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
 545 550 555 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
 610 615 620

gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt cgc 1913
 Ala Asp Glu Glu Glu Lys
 625 630

<210> 364

<211> 630

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp
 1 5 10 15

Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
 20 25 30

Gly	Phe	Phe	Ala	Pro	Tyr	Asn	Asp	Tyr	Ala	Ala	Asn	Lys	Asn	Pro	Gly	35	40	45
Gly	Ala	Val	Ala	Glu	Phe	Lys	Gly	Leu	Val	Arg	Ser	Tyr	His	Glu	Ala	50	55	60
Gly	Leu	Glu	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Glu	Gly	65	70	75
Asn	His	Met	Gly	Pro	Thr	Ile	Ala	Phe	Arg	Gly	Ile	Asp	Asn	Glu	Ala	85	90	95
Tyr	Tyr	Arg	Leu	Val	Glu	Gly	Asp	Arg	Arg	His	Tyr	Met	Asp	Tyr	Thr	100	105	110
Gly	Thr	Gly	Asn	Ser	Leu	Asn	Val	Arg	Asp	Pro	His	Ser	Leu	Gln	Leu	115	120	125
Ile	Met	Asp	Ser	Leu	Arg	Tyr	Trp	Val	Thr	Glu	Met	His	Val	Asp	Gly	130	135	140
Phe	Arg	Phe	Asp	Leu	Ala	Ser	Thr	Leu	Ala	Arg	Glu	Phe	Asp	Asp	Val	145	150	155
Asp	Arg	Leu	Ala	Thr	Phe	Phe	Asp	Leu	Val	Gln	Gln	Asp	Pro	Val	Val	165	170	175
Ser	Gln	Val	Lys	Leu	Ile	Ala	Glu	Pro	Trp	Asp	Val	Gly	Glu	Gly	Gly	180	185	190
Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	Glu	Trp	Asn	Gly	Lys	195	200	205
Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu	210	215	220
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn	225	230	235
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp	245	250	255
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met	260	265	270
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp	275	280	285
Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu	290	295	300
Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln	305	310	315
Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn	325	330	335
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn	340	345	350
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg			

355	360	365
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe 370	375	380
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala 385	390	395
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe 405	410	415
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu 420	425	430
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu 435	440	445
Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu 450	455	460
His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val 465	470	475
Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr 485	490	495
Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp 500	505	510
Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu 515	520	525
Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala 530	535	540
Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala 545	550	555
Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala 565	570	575
Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln 580	585	590
Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp 595	600	605
Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu 610	615	620
Ala Asp Glu Glu Glu Lys 625	630	

<210> 365

<211> 1496

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1473)

<223> FRXA01884

<400> 365

atg cat gtc gac ggc ttc cgc ttc gac ctt gcc tct acc ctt gct cgt	48
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg	
1 5 10 15	
gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa	96
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln	
20 25 30	
caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat	144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp	
35 40 45	
gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act	192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr	
50 55 60	
gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt	240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly	
65 70 75 80	
gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct	288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser	
85 90 95	
gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt	336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe	
100 105 110	
gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac	384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn	
115 120 125	
gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca	432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser	
130 135 140	
cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct	480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro	
145 150 155 160	
gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc	528
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr	
165 170 175	
ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg	576
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met	
180 185 190	
gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa	624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu	
195 200 205	
ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg	672
Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val	
210 215 220	
agc ttc acc agg cgt ttg ctg cgt atc cga gca aac cac cca gta ttt	720

Ser 225	Phe	Thr	Arg	Arg	Leu 230	Leu	Arg	Ile	Arg	Ala 235	Asn	His	Pro	Val	Phe 240	
agg Arg	cgc Arg	agg Arg	cag Gln	ttc Phe 245	ctt Leu	gcc Ala	ggt Gly	ggc Gly	cct Pro 250	ttg Leu	ggc Gly	gcc Ala	gat Asp	gtt Val 255	cgt Arg	768
gac Asp	cgc Arg	gat Asp	atc Ile 260	gca Ala	tgg Trp	ctg Leu	gta Val 265	cca Pro	aat Asn 265	gga Gly	acc Thr	ttg Leu 270	atg Met	act Thr	caa Gln	816
gat Asp	gac Asp	tgg Trp 275	gac Asp	ttc Phe	gct Ala	ttc Phe	ggt Gly 280	aaa Lys	tca Ser	ctg Leu	cag Gln	gtg Val 285	ttc Phe	ttc Phe	aac Asn	864
ggc Gly 290	gat Asp	gcc Ala	atc Ile	gaa Glu	gag Glu	cct Pro 295	gat Asp	tat Tyr	cga Arg	gga Gly	cag Gln	aaa Lys	atc Ile	cac His	gat Asp	912
gac Asp 305	tcc Ser	ttc Phe	atc Ile	ttg Leu	atg Met 310	ttc Phe	aac Asn	gct Ala	cac His	ttc Phe 315	gaa Glu	cct Pro	atc Ile	gat Asp	ttc Phe 320	960
aat Asn	ctc Leu	cct Pro	cct Pro	gag Glu 325	cat His	ttc Phe	ggt Gly	atg Met	aag Lys 330	tgg Trp	aag Lys	ctt Leu	ttg Leu	gtc Val	gat Asp 335	1008
acc Thr	acc Thr	gaa Glu	gcg Ala	gtg Val 340	ggc Gly	cac His	ccg Pro	ctg Leu	gag Glu	gat Asp	ctc Leu	acc Thr	atc Ile	gaa Glu	gct Ala	1056
ggc Gly	gga Gly	acc Thr 355	atc Ile	act Thr	gtt Val	cct Pro	gcc Ala 360	cgt Arg	tcc Ser	acg Thr	atg Met	ctg Leu	ctg Leu	cgc Arg	cag Gln	1104
gtg Val 370	gag Glu	gct Ala	ccg Pro	gac Asp	tac Tyr	acc Thr 375	aag Lys	ctt Leu	gag Glu	gaa Glu	aag Lys	atc Ile	gct Ala	gct Ala	gaa Glu	1152
aag Lys 385	cgt Arg	gag Glu	caa Gln	gaa Glu	ctt Leu 390	gcg Ala	gca Ala	gag Glu	aag Lys	gaa Glu 395	gct Ala	gct Ala	gag Glu	aag Lys	cgc Arg 400	1200
gaa Glu	ttg Leu	gaa Glu	ctg Leu	gcg Ala	gca Ala	gca Ala	aag Lys	gaa Glu	gct Ala	gaa Glu	gat Asp	gct Ala	gct Ala	gag Glu	gct Ala	1248
ctc Leu	cac His	ctt Leu	gcg Ala	gca Ala	gaa Glu	cgt Arg	gct Ala	tgc Ser	act Thr	cag Gln	gaa Glu	gct Ala	gaa Glu	ttg Leu	gcc Ala	1296
cat His	caa Gln	cac His	ggt Gly	gct Ala	gat Asp	gcg Ala	att Ile 440	gcc Ala	gat Asp	gag Glu	gta Val	gcg Ala	gaa Glu	gaa Glu	cca Pro	1344
caa Gln 450	gag Glu	ctg Leu	cca Pro	caa Gln	gat Asp	gaa Glu	gta Val	gcg Ala	gca Ala	gag Glu	gtc Val	gag Glu	act Thr	gag Glu	ccc Pro	1392
gac Asp	acc Thr	gag Glu	cct Pro	gac Asp	act Thr	gaa Glu	tct Ser	gac Asp	tcc Ser	gag Glu	cag Gln	gct Ala	gag Glu	gta Val	gct Ala	1440

465					470					475				480	
tca	gag	gag	cct	gaa	gcg	gac	gaa	gaa	gag	aag	tagtacaccg	aaagtggcgt	1493		
Ser	Glu	Glu	Pro	Glu	Ala	Asp	Glu	Glu	Glu	Lys					
				485					490						

cgc	1496
-----	------

```
<210> 366
<211> 491
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 366
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
1 5 10 15

Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
65 70 75 80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser
85 90 95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe
100 105 110

Val	Thr	Ala	His	Asp	Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn
		115				120						125			

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser
130 135 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro
145 150 155 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr
165 170 175

Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met
180 185 190

Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu
195 200 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val
210 215 220

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe
225 230 235 240

Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg

245								250				255			
Asp	Arg	Asp	Ile 260	Ala	Trp	Leu	Val	Pro 265	Asn	Gly	Thr	Leu	Met 270	Thr	Gln
Asp	Asp	Trp 275	Asp	Phe	Ala	Phe	Gly 280	Lys	Ser	Leu	Gln	Val 285	Phe	Phe	Asn
Gly	Asp 290	Ala	Ile	Glu	Glu	Pro 295	Asp	Tyr	Arg	Gly	Gln 300	Lys	Ile	His	Asp
Asp 305	Ser	Phe	Ile	Leu	Met 310	Phe	Asn	Ala	His	Phe 315	Glu	Pro	Ile	Asp	Phe 320
Asn	Leu	Pro	Pro	Glu 325	His	Phe	Gly	Met 330	Lys	Trp	Lys	Leu	Leu	Val 335	Asp
Thr	Thr	Glu	Ala 340	Val	Gly	His	Pro	Leu 345	Glu	Asp	Leu	Thr	Ile 350	Glu	Ala
Gly	Gly	Thr 355	Ile	Thr	Val	Pro	Ala 360	Arg	Ser	Thr	Met	Leu 365	Leu	Arg	Gln
Val 370	Glu	Ala	Pro	Asp	Tyr	Thr 375	Lys	Leu	Glu	Glu	Lys 380	Ile	Ala	Ala	Glu
Lys 385	Arg	Glu	Gln	Glu	Leu 390	Ala	Ala	Glu	Lys	Glu 395	Ala	Ala	Glu	Lys	Arg 400
Glu	Leu	Glu	Leu	Ala 405	Ala	Ala	Lys	Glu 410	Ala	Glu	Asp	Ala	Ala	Glu 415	Ala
Leu	His	Leu	Ala 420	Ala	Glu	Arg	Ala	Ser 425	Thr	Gln	Glu	Ala	Glu 430	Leu	Ala
His	Gln	His 435	Gly	Ala	Asp	Ala	Ile 440	Ala	Asp	Glu	Val	Ala 445	Glu	Glu	Pro
Gln	Glu 450	Leu	Pro	Gln	Asp	Glu 455	Val	Ala	Ala	Glu	Val 460	Glu	Thr	Glu	Pro
Asp 465	Thr	Glu	Pro	Asp	Thr 470	Glu	Ser	Asp	Ser	Glu 475	Gln	Ala	Glu	Val	Ala 480
Ser	Glu	Glu	Pro	Glu 485	Ala	Asp	Glu	Glu	Glu	Lys 490					

<210> 367

<211> 547

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA01111

<400> 367

aqaaaaccct gccgatgcaa actttgagga gagattcaat caaggaatag aaatcattct 60

ggtaggggtcta gacgcgcttg ggcatataag atgacgttcc											atg	aca	tca	acg	att	115			
											Met	Thr	Ser	Thr	Ile				
											1				5				
gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca															163				
Glu	His	Ser	Tyr	Gln	Val	Trp	Pro	Gly	His	Ala	Tyr	Pro	Leu	Gly	Ser				
				10					15					20					
acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca															211				
Thr	Tyr	Asp	Gly	Ala	Gly	Thr	Asn	Phe	Ala	Leu	Phe	Ser	Asp	Val	Ala				
				25					30					35					
gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga															259				
Glu	Arg	Val	Glu	Leu	Cys	Leu	Leu	Asp	Ala	Asp	Asn	Asn	Glu	Thr	Arg				
				40					45					50					
att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct															307				
Ile	Pro	Leu	Glu	Glu	Arg	Asp	Ala	His	Ile	Trp	His	Cys	Tyr	Leu	Pro				
				55					60					65					
ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg															355				
Gly	Val	Gln	Pro	Gly	Gln	Arg	Tyr	Gly	Phe	Arg	Val	His	Gly	Pro	Trp				
				70					75					80					
aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat															403				
Asn	Pro	Asp	Glu	Gly	Lys	Arg	Cys	Asp	Ala	Asn	Lys	Leu	Leu	Val	Asp				
				90					95					100					
ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta															451				
Pro	Tyr	Ala	Arg	Ala	Phe	Asp	Gly	Asp	Phe	Asp	Gly	His	Pro	Ser	Leu				
				105					110					115					
ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc															499				
Phe	Ser	Tyr	Asp	Ile	Thr	Asn	Pro	Asn	Asp	Pro	Asn	Gly	Arg	Asn	Thr				
				120					125					130					
gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc															547				
Glu	Asp	Ser	Ile	Asp	His	Thr	Met	Lys	Ser	Val	Val	Val	Asn	Pro	Phe				
				135					140					145					

<210> 368

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 368

Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala
1 5 10 15

Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu
20 25 30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp
35 40 45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp
50 55 60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg
65 70 75 80

[illegible]

```
<210> 369
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1612)
<223> RXN01550
```

<400> 369
ttcgccagca gtaatttttc acctctgctt ccttcgaggc catgattcag ggccacctgg 60

cgaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac 115
Val Gln Leu Asn Asp
1 5

act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac 163
Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp
10 15 20

gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc 211
Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr
25 30 35

ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg 259
Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp
 40 45 50

gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc 307
Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile
55 60 65

aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg 355
Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu
70 75 80 85

gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt 403
Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val
90 95 100

```
cat atg gca tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg 451
His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val
      105                      110                      115
```

gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg	499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp	
120 125 130	
tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc	547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
135 140 145	
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
150 155 160 165	
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg	643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
170 175 180	
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc	691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
185 190 195	
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
200 205 210	
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
215 220 225	
att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac	835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
295 300 305	
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc	1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly	
345 350 355	

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc 1219
 Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile
 360 365 370

ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag 1267
 Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu
 375 380 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac 1315
 Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp
 390 395 400 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac 1363
 Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr
 410 415 420

gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac 1411
 Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp
 425 430 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac 1459
 Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp
 440 445 450

cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg 1507
 Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met
 455 460 465

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635
 Val Lys Lys

<210> 370

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met
 1 5 10 15

Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65 70 75 80

527

Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn
 405 410 415
 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly
 420 425 430
 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr
 435 440 445
 Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu
 450 455 460
 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe
 465 470 475 480
 Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu
 485 490 495
 Glu Pro Thr Pro Ala Val Lys Lys
 500

<210> 371
 <211> 1367
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> FRXA01550

<400> 371
 atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc aca gag atc 48
 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
 1 5 10 15
 gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag 96
 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca 144
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg 192
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg 240
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt 288
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt 336
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110

tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	
gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat	720
Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp	
225 230 235 240	
cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac	768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn	
245 250 255	
gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag	816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln	
260 265 270	
att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc	864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe	
275 280 285	
atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta	912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val	
290 295 300	
gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct	960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala	
305 310 315 320	
cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag	1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu	
325 330 335	
ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat	1056
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp	
340 345 350	
aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag	1104

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aag 1344
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445
 taggttttaa cctccgcttc taa 1367

 <210> 372
 <211> 448
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 372
 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
 1 5 10 15
 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110
 Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
 115 120 125
 Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
 130 135 140
 Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
 145 150 155 160

Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
 165 170 175
 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
 180 185 190
 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
 195 200 205
 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
 210 215 220
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
 225 230 235 240
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
 275 280 285
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
 290 295 300
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
 305 310 315 320
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
 325 330 335
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
 340 345 350
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445

<210> 373

<211> 2348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc	48
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser	
1 5 10 15	
gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	
tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
ggt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344
Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met	
435 440 445	
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392

Leu Arg Asn Pro Glu Arg	Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg	
450	455	460
cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt		1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly		
465	470	475 480
ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt		1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly		
	485	490 495
gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc		1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala		
	500	505 510
agc tac ctg atc tct ggt gct gac gtc tgg ctg aac aac cca gtg cgc		1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg		
	515	520 525
cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt		1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly		
	530	535 540
ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag		1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys		
	545	550 555 560
gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa		1728
Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu		
	565	570 575
tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac		1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn		
	580	585 590
gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag		1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln		
	595	600 605
gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg		1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met		
	610	615 620
gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc		1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg		
	625	630 635 640
cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg		1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala		
	645	650 655
gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc		2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val		
	660	665 670
aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag		2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu		
	675	680 685
ctt gaa gtc agc gtt cgc gtt gat tcc ggt tcg ctt aac gac gac gag		2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu		

690	695	700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc			2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile			
705	710	715	720
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac			2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr			
	725	730	735
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc			2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala			
	740	745	750
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc			2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg			
	755	760	765
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa			2348
Leu Ile Thr Tyr Leu Glu Asn			
	770	775	
 <210> 374			
<211> 775			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 374			
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser			
1	5	10	15
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly			
	20	25	30
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser			
	35	40	45
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met			
	50	55	60
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu			
	65	70	75
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln			
	85	90	95
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala			
	100	105	110
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro			
	115	120	125
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg			
	130	135	140
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu			
	145	150	155
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg			
	165	170	175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
 405 410 415
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
 420 425 430
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
 435 440 445
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
 450 455 460
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
 465 470 475 480
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
 485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
 500 505 510
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
 515 520 525
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
 530 535 540
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
 545 550 555 560
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
 565 570 575
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
 580 585 590
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
 595 600 605
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
 610 615 620
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
 625 630 635 640
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
 645 650 655
 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
 660 665 670
 Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
 675 680 685
 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
 690 695 700
 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
 705 710 715 720
 Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
 725 730 735
 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
 740 745 750
 Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg
 755 760 765
 Leu Ile Thr Tyr Leu Glu Asn
 770 775

<210> 375

<211> 941

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(918)

<223> FRXA02100

<400> 375

att gct ggt aag gca cac cca cat gac atg ggt ggc aag aag ctc atg	48
Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met	
1 5 10 15	
cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	
aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt	672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val	
210 215 220	

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240
 ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255
 acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270
 act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285
 aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300
 gag aac tagggcgaaa ctagctttac caa 941
 Glu Asn
 305

<210> 376

<211> 306

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met
 1 5 10 15
 Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe
 20 25 30
 Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
 35 40 45
 Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
 50 55 60
 Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
 65 70 75 80
 Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
 85 90 95
 Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110
 Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125
 Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140
 Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

Glu Asn
 305

<210> 377

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1206)

<223> FRXA02113

<400> 377

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc 48
 Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
 1 5 10 15

gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
ggt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 gct cgc 1206
 Ala Arg

<210> 378

<211> 402

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 378

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
 1 5 10 15
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg

<210> 379

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA02147

<400> 379

aaaagttgag agcggcttgc ttcttttccct tggctaggct tttgtaatcg ggtagagta 60

gtggagttgc ttgaatgagg ttgatagggg atttttgaag atg ttt ggt cgc cgt	115
Met Phe Gly Arg Arg	
1 5	
tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg	163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu	
10 15 20	
gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat	211
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp	
25 30 35	
atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa	259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys	
40 45 50	
cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt	307
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val	
55 60 65	
cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag	355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu	
70 75 80 85	
aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag	403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys	
90 95 100	
tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa	451
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu	
105 110 115	
gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act	499
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr	
120 125 130	
aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag	547
Lys Ser Thr Ser Asp Val Glu Ser Leu Asn Ala Glu Thr Glu Lys	
135 140 145	
tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag	595
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu	
150 155 160 165	
ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa	643
Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu	
170 175 180	
aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat	691
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp	
185 190 195	
gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca	739
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro	
200 205 210	
ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg	787
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser	
215 220 225	

ggt gcg gtg gat gct gcc ttg tct aag ttg gga agc cct tat ggt tgg 835
 Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp
 230 235 240 245
 ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg 883
 Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp
 250 255 260
 gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag 931
 Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln
 265 270 275
 atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat 979
 Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp
 280 285 290
 gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg 1027
 Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly
 295 300 305
 gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg 1075
 Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val
 310 315 320 325
 gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac 1117
 Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala Arg Arg Tyr
 330 335
 taagaaatag ttcgtcagga gaa 1140

<210> 380

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Phe Gly Arg Arg Trp Val Ser Val Val Ala Ser Cys Val Ile Ala
 1 5 10 15
 Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp
 20 25 30
 Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln
 35 40 45
 Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
 50 55 60
 Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65 70 75 80
 Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
 85 90 95
 Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
 100 105 110
 Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
 130 135 140
 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
 145 150 155 160
 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
 165 170 175
 Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
 180 185 190
 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
 195 200 205
 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
 210 215 220
 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
 225 230 235 240
 Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
 245 250 255
 Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
 260 265 270
 Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu
 275 280 285
 Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val
 290 295 300
 Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly
 305 310 315 320
 Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala
 325 330 335

Arg Arg Tyr

<210> 381
 <211> 1959
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1936)
 <223> RXA01478

<400> 381
 gcgggttttg ttgtggaggg gcgcgtcgaa aagcaatttt tttccaaga tagctcactt 60
 tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115
 Met Thr Ile Pro Gly
 1 5
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163

Ala	Ser	Thr	Gln	Thr	Asp	Ile	Pro	Leu	Asp	Thr	Leu	Leu	Glu	Asp	Tyr	
				10					15					20		
gcg	cta	ctg	tca	gac	act	cac	acc	ggc	gct	ctg	ctg	tcc	aac	atg	ggc	211
Ala	Leu	Leu	Ser	Asp	Thr	His	Thr	Gly	Ala	Leu	Leu	Ser	Asn	Met	Gly	
			25					30					35			
agt	ttg	gac	tgg	ttg	tgc	ctg	cct	cgt	ttt	gat	tcc	caa	gcc	atg	ttc	259
Ser	Leu	Asp	Trp	Leu	Cys	Leu	Pro	Arg	Phe	Asp	Ser	Gln	Ala	Met	Phe	
		40					45					50				
acc	agg	ctg	ctt	ggt	gat	cgc	gag	cac	gga	cac	tgg	agt	ttg	cgt	gtc	307
Thr	Arg	Leu	Leu	Gly	Asp	Arg	Glu	His	Gly	His	Trp	Ser	Leu	Arg	Val	
	55					60					65					
cca	ggt	ggt	gag	gtg	atc	agc	caa	aac	tac	ctc	ggc	gat	tcc	ttc	gtg	355
Pro	Gly	Gly	Glu	Val	Ile	Ser	Gln	Asn	Tyr	Leu	Gly	Asp	Ser	Phe	Val	
70					75					80					85	
gtg	cag	acc	gtg	tgg	cgt	tca	gag	acc	ggt	act	gcc	cgg	gtt	gtt	gat	403
Val	Gln	Thr	Val	Trp	Arg	Ser	Glu	Thr	Gly	Thr	Ala	Arg	Val	Val	Asp	
				90					95					100		
ttc	atg	cca	att	cac	ggt	caa	gaa	caa	ccc	gat	atc	acc	gac	ctg	gtg	451
Phe	Met	Pro	Ile	His	Gly	Gln	Glu	Gln	Pro	Asp	Ile	Thr	Asp	Leu	Val	
			105					110					115			
cgc	tct	gtg	cac	tgc	gtg	gaa	ggc	gaa	gtg	gat	gtg	gaa	tcg	atc	ctg	499
Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu	
		120					125					130				
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser	
	135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala	
150					155					160					165	
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys	
				170					175					180		
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val	
			185					190					195			
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr	
		200					205					210				
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu	
	215					220					225					
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met	
230					235					240					245	
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggt	ggc	atc	gtg	gcc	883
Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala	

250								255					260					
gca	ccg	acc	acc	tca	cta	cca	gag	gat	ttc	gga	ggc	atc	cgt	aac	tgg	931		
Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp			
265								270				275						
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc	979		
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala			
280								285				290						
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg	1027		
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp			
295												305						
ctg	ctg	cgc	gcc	atc	gca	ggc	gac	ccg	gaa	aac	ctc	cgc	atc	atg	tat	1075		
Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn	Leu	Arg	Ile	Met	Tyr			
310				315								320				325		
ggc	ctc	ggc	ggc	gaa	cga	cac	ctc	cct	gaa	cgc	gaa	ctc	caa	cac	ctg	1123		
Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu			
				330								335				340		
cgc	gga	tac	gaa	aac	tcc	gtg	cct	gtt	cgc	gtt	ggc	aat	gga	gcc	gcc	1171		
Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val	Gly	Asn	Gly	Ala	Ala			
				345								350				355		
gaa	caa	tac	caa	gca	gat	gtc	gtc	ggc	gaa	gta	atg	gtc	gcg	ctt	gaa	1219		
Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val	Met	Val	Ala	Leu	Glu			
				360								365				370		
acc	atc	cgc	cgc	gcc	ggg	tgc	ctc	gag	gac	gaa	ttc	tcc	tgg	ggc	atg	1267		
Thr	Ile	Arg	Arg	Ala	Gly	Cys	Leu	Glu	Asp	Glu	Phe	Ser	Trp	Gly	Met			
375												380				385		
caa	aaa	gcc	atc	ctc	gat	ttc	caa	gaa	gcc	aac	ttc	gac	cgc	aag	gat	1315		
Gln	Lys	Ala	Ile	Leu	Asp	Phe	Gln	Glu	Ala	Asn	Phe	Asp	Arg	Lys	Asp			
390				395								400				405		
caa	ggc	atc	tgg	gaa	atg	cgc	tcc	gaa	ccg	caa	tat	ttc	acc	cac	ggc	1363		
Gln	Gly	Ile	Trp	Glu	Met	Arg	Ser	Glu	Pro	Gln	Tyr	Phe	Thr	His	Gly			
				410				415								420		
cgc	gcc	atg	atg	tgg	gcc	ggc	ttc	gac	cgc	ggc	atc	aaa	gcc	atc	gaa	1411		
Arg	Ala	Met	Met	Trp	Ala	Gly	Phe	Asp	Arg	Gly	Ile	Lys	Ala	Ile	Glu			
				425				430								435		
gaa	ttc	aac	ctc	gac	ggc	ccc	atc	gag	cgc	tgg	cgt	gaa	ctc	cgc	gcc	1459		
Glu	Phe	Asn	Leu	Asp	Gly	Pro	Ile	Glu	Arg	Trp	Arg	Glu	Leu	Arg	Ala			
				440				445				450						
aaa	ctc	cgc	gaa	gaa	atc	atg	acc	aac	ggc	ttc	aac	gaa	gag	atc	caa	1507		
Lys	Leu	Arg	Glu	Glu	Ile	Met	Thr	Asn	Gly	Phe	Asn	Glu	Glu	Ile	Gln			
455								460				465						
tcc	ttc	acc	cag	tgc	tac	gac	aac	acc	caa	gtc	gac	gcc	tcg	ctg	ctt	1555		
Ser	Phe	Thr	Gln	Cys	Tyr	Asp	Asn	Thr	Gln	Val	Asp	Ala	Ser	Leu	Leu			
470				475								480				485		
cag	ctc	gcc	caa	ata	ggc	ttc	atc	ggc	ttc	gac	gat	cca	aaa	atg	ctc	1603		
Gln	Leu	Ala	Gln	Ile	Gly	Phe	Ile	Gly	Phe	Asp	Asp	Pro	Lys	Met	Leu			
				490								495				500		

agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt 1651
 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe
 505 510 515
 ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu
 520 525 530
 tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser
 535 540 545
 tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala
 550 555 560 565
 gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His
 570 575 580
 ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu
 585 590 595
 atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg 1936
 Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg
 600 605 610
 tagagtctaa ggtgtcattc ttg 1959

<210> 382

<211> 612

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Thr Ile Pro Gly Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr
 1 5 10 15
 Leu Leu Glu Asp Tyr Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu
 20 25 30
 Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp
 35 40 45
 Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
 50 55 60
 Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65 70 75 80
 Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
 85 90 95
 Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
 100 105 110
 Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
 130 135 140
 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
 145 150 155 160
 Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
 165 170 175
 Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
 180 185 190
 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
 195 200 205
 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
 210 215 220
 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
 225 230 235 240
 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
 245 250 255
 Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
 260 265 270
 Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
 275 280 285
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
 290 295 300
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
 305 310 315 320
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
 325 330 335
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
 340 345 350
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
 355 360 365
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
 370 375 380
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
 385 390 395 400
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
 405 410 415
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
 420 425 430
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
 435 440 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
 450 455 460
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
 465 470 475 480
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
 485 490 495
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
 500 505 510
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
 515 520 525
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
 530 535 540
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
 545 550 555 560
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
 565 570 575
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
 580 585 590
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu
 595 600 605
 Ala Arg Asn Arg
 610

<210> 383
 <211> 658
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXA01888

<400> 383
 agtagatact agataccacc cattgatgcc gtcaaggggt ttcctgtaaa gatgtaagag 60
 attaagaaaa gaggtagata tggcgtcaaaa gcgaccgaca atg gct gat gtg gca 115
 Met Ala Asp Val Ala
 1 5
 aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
 10 15 20
 gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
 Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
 25 30 35
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln

40	45	50	
aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc			307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe			
55	60	65	
cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc			355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly			
70	75	80	85
ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat			403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp			
90	95	100	
gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta			451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu			
105	110	115	
gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt			499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu			
120	125	130	
ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc			547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser			
135	140	145	
gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc			595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu			
150	155	160	165
atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc			643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala			
170	175	180	
cct ggc acc cag gaa			658
Pro Gly Thr Gln Glu			
185			

<210> 384

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met	Ala	Asp	Val	Ala	Lys	Ala	Ala	Gly	Val	Ser	Thr	Ala	Leu	Val	Ser
1				5					10					15	

Ile	Val	Phe	Arg	Asp	Ala	Pro	Gly	Ala	Ser	Glu	Ser	Thr	Arg	Asn	His
		20					25						30		

Val	Lys	Glu	Lys	Ala	Ala	Glu	Leu	Gly	Tyr	Ile	Pro	Asp	Arg	Arg	Ala
	35					40						45			

Gln	Lys	Leu	Arg	Gln	Asn	Arg	Ser	Gly	Leu	Ile	Gly	Val	Ala	Phe	Glu
	50					55					60				

Met	His	Gln	Ala	Phe	His	Gly	Asp	Ile	Val	Glu	His	Leu	Tyr	Pro	Thr
65					70					75				80	

Ala	Arg	Lys	His	Gly	Phe	Asp	Leu	Tyr	Leu	Ser	Ala	Ile	Thr	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	85		90		95
Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu	100		105		110
Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr	115		120		125
Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr	130		135		140
Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu	145		150		155
Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile	165		170		175
Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu	180		185		

<210> 385

<211> 1503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1480)

<223> RXN01927

<400> 385

gagcagcggg atcttttgcg taattcgcg gcgcagatcc atgtgattga ccacaatggt 60

gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt	115
Met Ala Leu Val Leu	
1 5	

gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc	163
Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala	
10 15 20	

gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg	211
Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly	
25 30 35	

tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc	259
Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr	
40 45 50	

gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag	307
Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln	
55 60 65	

cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg	355
His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala	
70 75 80 85	

ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat	403
Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn	
90 95 100	

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg 1171
 Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu
 345 350 355
 gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag 1219
 Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln
 360 365 370
 cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag 1267
 Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu
 375 380 385
 att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct 1315
 Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala
 390 395 400 405
 gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg 1363
 Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser
 410 415 420
 ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac 1411
 Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His
 425 430 435
 cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt 1459
 Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg
 440 445 450
 gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa 1503
 Ala Ala Thr Gln Gly Trp Tyr
 455 460

<210> 386

<211> 460

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

Met Ala Leu Val Leu Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala
 1 5 10 15

Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala
 20 25 30

Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
 35 40 45

Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
 50 55 60

Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
 65 70 75 80

Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
 85 90 95

Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
 100 105 110

Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

115	120	125
Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val 130 135 140		
Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg 145 150 155 160		
Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr 165 170 175		
Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His 180 185 190		
Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr 195 200 205		
Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala 210 215 220		
Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile 225 230 235 240		
Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp 245 250 255		
Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe 260 265 270		
Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg 275 280 285		
Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala 290 295 300		
Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly 305 310 315 320		
Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu 325 330 335		
Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly 340 345 350		
Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr 355 360 365		
Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser 370 375 380		
Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val 385 390 395 400		
Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala 405 410 415		
Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro 420 425 430		
Gly Ser Asp Pro His Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg 435 440 445		

Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr
 450 455 460

<210> 387
 <211> 1139
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1116)
 <223> FRXA01927

<400> 387
 aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat gag gag atc 48
 Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
 1 5 10 15
 ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc 192
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct 240
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat 288
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg 336
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct 384
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag 432
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg 480
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc 528
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc 576

Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly	
180 185 190	
gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa	624
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu	
195 200 205	
gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg	672
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val	
210 215 220	
acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca	720
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala	
225 230 235 240	
gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac	768
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp	
245 250 255	
ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct	816
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala	
260 265 270	
gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag	864
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln	
275 280 285	
ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct	912
Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro	
290 295 300	
gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg	960
Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val	
305 310 315 320	
gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc	1008
Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala	
325 330 335	
acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct	1056
Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro	
340 345 350	
aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg	1104
Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr	
355 360 365	
cag ggt tgg tac tagagctcga tattgtcgat caa	1139
Gln Gly Trp Tyr	
370	

<210> 388

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
1 5 10 15

Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
 180 185 190
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
 195 200 205
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
 210 215 220
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
 225 230 235 240
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
 245 250 255
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
 260 265 270
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
 275 280 285
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
 290 295 300
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
 305 310 315 320
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
 325 330 335
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro

340 345 350
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
 355 360 365
 Gln Gly Trp Tyr
 370
 <210> 389
 <211> 844
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA02729
 <400> 389
 gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60
 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115
 Met Asp Ser Pro Met
 1 5
 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala
 10 15 20
 gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211
 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu
 25 30 35
 ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259
 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln
 40 45 50
 gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307
 Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala
 55 60 65
 gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355
 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln
 70 75 80 85
 tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403
 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly
 90 95 100
 ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451
 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val
 105 110 115
 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499
 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His
 120 125 130
 tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile
 135 140 145

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val
 150 155 160 165

 gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg
 170 175 180

 cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu
 185 190 195

 gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc 739
 Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val
 200 205 210

 act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly
 215 220 225

 gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro
 230 235 240 245

 acc cca aag 844
 Thr Pro Lys

<210> 390
 <211> 248
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 390
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val
 1 5 10 15

 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu
 20 25 30

 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly
 35 40 45

 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val
 50 55 60

 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu
 65 70 75 80

 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val
 85 90 95

 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu
 100 105 110

 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu
 115 120 125

 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130	135	140
Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu		
145	150	155 160
Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly		
	165	170 175
His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu		
	180	185 190
Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp		
	195	200 205
Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val		
	210	215 220
Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln		
	225	230 235 240
Leu Thr Ala Ile Pro Thr Pro Lys		
	245	

<210> 391
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1003)
 <223> RXA02797

<400> 391
 acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60
 ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115
 Met Asn Asn Arg Ile
 1 5
 gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163
 Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg
 10 15 20
 cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211
 His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr
 25 30 35
 gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259
 Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly
 40 45 50
 gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307
 Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala
 55 60 65
 cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta 355
 Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val
 70 75 80 85

tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa	403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys	
90 95 100	
gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc	451
Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val	
105 110 115	
aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga	499
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly	
120 125 130	
atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc	547
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala	
135 140 145	
att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc	595
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile	
150 155 160 165	
gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat	643
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn	
170 175 180	
gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat	691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp	
185 190 195	
tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc	739
Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe	
200 205 210	
gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat	787
Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp	
215 220 225	
gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac	835
Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp	
230 235 240 245	
acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta	883
Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu	
250 255 260	
att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc	931
Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val	
265 270 275	
ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac	979
Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp	
280 285 290	
gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg	1026
Ala Ser Val Ser Leu Pro Ser Val	
295 300	

<210> 392

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
 1 5 10 15

Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
 20 25 30

Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
 35 40 45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
 50 55 60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
 65 70 75 80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
 85 90 95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
 100 105 110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
 115 120 125

Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
 130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
 145 150 155 160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
 165 170 175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
 180 185 190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
 195 200 205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
 210 215 220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
 225 230 235 240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
 245 250 255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
 260 265 270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
 275 280 285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val
 290 295 300

<210> 393

<211> 1161
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1138)
 <223> RXA02730

<400> 393

```

ccaacatcgc cttgcacgta atagggttaaa acacaagtga atgtaatcgt ttgcagcaat 60

cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115
                                   Met Ala Thr Glu Lys
                                   1 5

ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
                                   10 15 20

gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
                                   25 30 35

act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
                                   40 45 50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt 307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly
                                   55 60 65

gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act 355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr
                                   70 75 80 85

gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc 403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr
                                   90 95 100

aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc 451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu
                                   105 110 115

acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc 499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys
                                   120 125 130

gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg 547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu
                                   135 140 145

gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct 595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser
                                   150 155 160 165

aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac 643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn
                                   170 175 180

aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca 691

```


Asn	Ala	Leu	Pro	Ile	Gly	Tyr	Leu	Ser	Gly	Pro	Met	Asp	Thr	Ser	Thr		
			185					190					195				
ggt	aga	gag	cga	tta	gag	gat	ttc	aaa	gca	gcc	tgc	gcc	aac	tcc	aaa	739	
Gly	Arg	Glu	Arg	Leu	Glu	Asp	Phe	Lys	Ala	Ala	Cys	Ala	Asn	Ser	Lys		
		200					205					210					
att	ggc	gaa	cag	ctc	gtt	ttt	ctg	ggt	ggg	tac	gaa	caa	agc	gtt	gga	787	
Ile	Gly	Glu	Gln	Leu	Val	Phe	Leu	Gly	Gly	Tyr	Glu	Gln	Ser	Val	Gly		
	215					220				225							
ttt	gaa	ggc	gct	acg	aaa	ttg	ctc	gat	caa	gga	gct	aaa	act	ctt	ttt	835	
Phe	Glu	Gly	Ala	Thr	Lys	Leu	Leu	Asp	Gln	Gly	Ala	Lys	Thr	Leu	Phe		
230					235					240					245		
gcc	ggc	gat	tct	atg	atg	acg	atc	ggt	gtc	att	gaa	gcc	tgc	cat	aag	883	
Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Val	Ile	Glu	Ala	Cys	His	Lys		
				250					255					260			
gct	ggt	ttg	gtt	atc	ggc	aag	gat	gtc	agc	gtg	att	ggt	ttt	gat	aca	931	
Ala	Gly	Leu	Val	Ile	Gly	Lys	Asp	Val	Ser	Val	Ile	Gly	Phe	Asp	Thr		
			265				270						275				
cat	ccg	ctt	ttt	gcc	ctg	caa	cct	cat	ccg	ttg	aca	gtg	att	gat	caa	979	
His	Pro	Leu	Phe	Ala	Leu	Gln	Pro	His	Pro	Leu	Thr	Val	Ile	Asp	Gln		
		280					285					290					
aat	gta	gaa	caa	cta	gcc	caa	cga	gca	gtg	tct	atc	ctc	acc	gaa	tta	1027	
Asn	Val	Glu	Gln	Leu	Ala	Gln	Arg	Ala	Val	Ser	Ile	Leu	Thr	Glu	Leu		
	295					300					305						
att	gca	ggc	acg	gta	cct	agc	gtg	acg	aaa	act	acg	atc	ccc	act	gcc	1075	
Ile	Ala	Gly	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr	Thr	Ile	Pro	Thr	Ala		
310					315					320					325		
ctt	att	cat	cgt	gaa	tca	atc	atc	aac	tcc	act	tta	agg	aag	aag	gat	1123	
Leu	Ile	His	Arg	Glu	Ser	Ile	Ile	Asn	Ser	Thr	Leu	Arg	Lys	Lys	Asp		
				330					335					340			
gga	ctc	ccc	aat	gag	taactcaacc	ggtaccgaca	ttg									1161	
Gly	Leu	Pro	Asn	Glu													
			345														

<210> 394

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met	Ala	Thr	Glu	Lys	Phe	Arg	Pro	Thr	Leu	Lys	Asp	Val	Ala	Arg	Gln		
1				5					10					15			

Ala	Gly	Val	Ser	Ile	Ala	Thr	Ala	Ser	Arg	Ala	Leu	Ala	Asp	Asn	Pro		
		20						25					30				

Ala	Val	Ala	Ala	Ser	Thr	Arg	Glu	Arg	Ile	Gln	Gln	Leu	Ala	Ser	Asp		
	35						40					45					

Leu	Gly	Tyr	Arg	Ala	Asn	Ala	Gln	Ala	Arg	Ala	Leu	Arg	Ser	Ser	Arg		
	50					55					60						

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65 70 75 80
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
 85 90 95
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
 100 105 110
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
 115 120 125
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
 130 135 140
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
 145 150 155 160
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
 165 170 175
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
 180 185 190
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
 195 200 205
 Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
 210 215 220
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
 225 230 235 240
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
 245 250 255
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
 260 265 270
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
 275 280 285
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
 290 295 300
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
 305 310 315 320
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
 325 330 335
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu
 340 345

<210> 395

<211> 483

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(460)

<223> RXA02551

<400> 395

gctgcacaaa ttccgcgaaa gggatatcacc atcgacatca cagatgaaga ccgtgagatc 60

ttaaaaaaac accgtcgatt tcatttcctt ctcctattac atg tcc gta tgt gaa 115
Met Ser Val Cys Glu
1 5

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly
10 15 20

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val
25 30 35

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp
40 45 50

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val
55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile
70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys
90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser
105 110 115

ctg gaa tcc taagaaataa aggtaggtgt cac 483
Leu Glu Ser
120

<210> 396

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly
1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu
20 25 30

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn
35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu

50					55					60					
Gly	Ala	Lys	Asp	Val	Leu	Ile	Asp	Gly	Pro	Ser	Gly	Pro	Thr	Val	Asn
65					70					75					80
Asp	Asp	Tyr	Arg	Ile	Lys	Tyr	Leu	Asp	Asp	Gly	Gly	Ser	Gly	Ile	Leu
				85					90					95	
Lys	Arg	Tyr	Lys	Lys	Lys	Ser	Phe	Asp	Trp	Cys	Arg	Asp	Ile	Ile	Ala
			100					105					110		
Thr	Asn	Gly	Glu	Ser	Leu	Glu	Ser								
		115					120								

```
<210> 397
<211> 795
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(772)  
<223> RXA01325
```

<400> 397																
gcgcagcgcgt	cggaacgatta	cgaacttcag	gagaactcgg		ggtcattcgt	tgcaattctac	60									
cctggaaaatt ttcccacact aagtcagggtc taagtaggggt atg gat atg acg att 115																
Met Asp Met Thr Ile 5																
1																
tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163																
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro																
10 15 20																
gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211																
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu																
25 30 35																
ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259																
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr																
40 45 50																
gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307																
Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe																
55 60 65																
ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355																
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu																
70 75 80 85																
gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403																
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala																
90 95 100																
gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451																
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala																
105 110 115																
atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc qaa 499																

Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu
 120 125 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg 547
 Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu
 135 140 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca 595
 Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro
 150 155 160 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct 643
 Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser
 170 175 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa 691
 Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu
 185 190 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct 739
 Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser
 200 205 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttgccg ttctaatacgg 792
 Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
 215 220

gac 795

<210> 398

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr
 1 5 10 15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile
 20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser
 35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala
 50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala
 65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val
 85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu
 100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr

130	135	140
Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser		
145	150	155
Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val		
	165	170
Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly		
	180	185
Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr		
195	200	205
Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu		
210	215	220

<210> 399
 <211> 684
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(661)
 <223> RXA00195

<400> 399
 tcgcagtcacat catgcaggca taacctgaaa cccatccggtt tggattgccc caaatgggtg 60
 tagtgggtgc gtttacccaa caagtgcagg aatgggagtc gtg act aaa aag atc 115
 Val Thr Lys Lys Ile
 1 5
 ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163
 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val
 10 15 20
 att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211
 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly
 25 30 35
 ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259
 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu
 40 45 50
 gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307
 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Val Ile
 55 60 65
 tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355
 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys
 70 75 80 85
 att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403
 Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val
 90 95 100

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451
 Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
 105 110 115
 cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499
 His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
 120 125 130
 gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547
 Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
 135 140 145
 cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595
 His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
 150 155 160 165
 gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643
 Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
 170 175 180
 ggg aga aga tgt ggg agg tgactcccgga gcaggcagca gcg 684
 Gly Arg Arg Cys Gly Arg
 185

<210> 400

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr
 1 5 10 15
 Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val
 20 25 30
 Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala
 35 40 45
 Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
 50 55 60
 Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly
 65 70 75 80
 Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val
 85 90 95
 Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr
 100 105 110
 Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
 115 120 125
 Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile
 130 135 140
 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly
 145 150 155 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro
 165 170 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg
 180 185

<210> 401

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA00196

<400> 401

ctgccatggc gcagtgtttg cgttcgggta ctctgatga gggtgcgcgg attgtgctga 60

cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act 115
 Met Trp Glu Val Thr
 1 5

ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163
 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn
 10 15 20

acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211
 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu
 25 30 35

gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259
 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val
 40 45 50

cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg 307
 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala
 55 60 65

acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355
 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu
 70 75 80 85

gcg ctt gat tgg cca cat cgg gtg ccg aag gct cag ccg gcg ctg gat 403
 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp
 90 95 100

ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451
 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala
 105 110 115

ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499
 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr
 120 125 130

tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt 547
 Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe
 135 140 145

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu
 150 155 160 165

 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp
 170 175 180

 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu
 185 190 195

 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738
 Ile Asn Arg Leu Ala Thr Asn Leu
 200 205

<210> 402

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 402

Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala
 1 5 10 15

 Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly
 20 25 30

 Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu
 35 40 45

 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr
 50 55 60

 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys
 65 70 75 80

 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala
 85 90 95

 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro
 100 105 110

 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala
 115 120 125

 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu
 130 135 140

 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val
 145 150 155 160

 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val
 165 170 175

 Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala
 180 185 190

 Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu
 195 200 205

<210> 403
 <211> 2031
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2008)
 <223> RXN01562

<400> 403

```
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtagaa 60
ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115
                                     Met Gly Ile Leu Asn
                                     1 5
agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                                     10 15 20
gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
                                     25 30 35
gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
                                     40 45 50
atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
                                     55 60 65
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
                                     70 75 80 85
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
                                     90 95 100
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
                                     105 110 115
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
                                     120 125 130
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
                                     135 140 145
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
                                     150 155 160 165
gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
```


acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg 1411
 Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu
 425 430 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat 1459
 Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp
 440 445 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc 1507
 Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro
 455 460 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct 1555
 Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala
 470 475 480 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc 1603
 Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala
 490 495 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg 1651
 Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala
 505 510 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa 1699
 Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys
 520 525 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro
 535 540 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile
 550 555 560 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser
 570 575 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala
 585 590 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala
 600 605 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp
 615 620 625

ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg 2031
 Leu Asp Ser Leu Phe Gly Glu
 630 635

<210> 404

<211> 636

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

```

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
 1           5           10           15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
          20           25           30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
      35           40           45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
      50           55           60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65           70           75           80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
          85           90           95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
      100           105           110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
      115           120           125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
      130           135           140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
145           150           155           160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
          165           170           175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
      180           185           190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys
      195           200           205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala
      210           215           220

Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu
225           230           235           240

Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His
          245           250           255

Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp
          260           265           270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala
      275           280           285

Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
      290           295           300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr

```

305	310	315	320
Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn	325	330	335
Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys	340	345	350
Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu	355	360	365
Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His	370	375	380
Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln	385	390	395
Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu	405	410	415
Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val	420	425	430
Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala	435	440	445
Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser	450	455	460
Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro	465	470	475
Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu	485	490	495
Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser	500	505	510
Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val	515	520	525
Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro	530	535	540
Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp	545	550	555
His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val	565	570	575
Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro	580	585	590
Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg	595	600	605
Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr	610	615	620
Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu	625	630	635

<210> 405
 <211> 1061
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1038)
 <223> FRXA01562

<400> 405
 gag cag gat ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg 48
 Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
 1 5 10 15
 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
 20 25 30
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60
 gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac 240
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg 288
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc 336
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc 384
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat 432
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt 480
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat 528
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190

```

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat      624
Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
      195                      200                      205

gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc      672
Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
      210                      215                      220

atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc      720
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
      225                      230                      235                      240

agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg      768
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
      245                      250                      255

att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac      816
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
      260                      265                      270

ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc      864
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
      275                      280                      285

ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga      912
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
      290                      295                      300

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa      960
Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
      305                      310                      315                      320

gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt      1008
Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
      325                      330                      335

gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg      1058
Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
      340                      345

ccg                                                                    1061

<210> 406
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 406
Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
  1                      5                      10                      15

Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
      20                      25                      30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
      35                      40                      45

Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
      50                      55                      60

```


Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
 210 215 220
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
 225 230 235 240
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
 245 250 255
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
 260 265 270
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
 275 280 285
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
 290 295 300
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
 305 310 315 320
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 340 345

<210> 407

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA01705

<400> 407

```

gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtaaa 60
ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115
                                   Met Gly Ile Leu Asn
                                   1 5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                                   10 15 20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
                                   25 30 35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
                                   40 45 50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
                                   55 60 65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
                                   70 75 80 85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
                                   90 95 100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
                                   105 110 115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
                                   120 125 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
                                   135 140 145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
                                   150 155 160 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
                                   170 175 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
                                   185 190 195

cct ttc tat gat 703
Pro Phe Tyr Asp

```

200

<210> 408

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
 1 5 10 15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
 85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
 100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
 165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
 180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp
 195 200

<210> 409

<211> 2241

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2218)

<223> RXN00879

<400> 409

caccccaaag cccaatccaa aagatgtatt ttctaacaaa cttaccctca cgctacaaat 60

atgctgtgcc cacacgctat tagtggcata atgttgtgtt	gtg act gct cgc aga	115
	Val Thr Ala Arg Arg	5
	1	
ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act		163
Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr		
	10 15 20	
gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa		211
Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys		
	25 30 35	
atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac		259
Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn		
	40 45 50	
gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc		307
Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe		
	55 60 65	
act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta		355
Thr Arg Pro Leu Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu		
	70 75 80 85	
gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc		403
Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile		
	90 95 100	
gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg		451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp		
	105 110 115	
aca gcg cca cgg gaa att gat ggg att agg tgg ggc gag gca tcg ttt		499
Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe		
	120 125 130	
aag att cct ggt gat ctc ccc ttg ggt tgg cac aag ctt cac ctt aaa		547
Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys		
	135 140 145	
tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt		595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg		
	150 155 160 165	
ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg		643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met		
	170 175 180	
gcg cag atc tac tct gtg cgt tcc acg ttg tcg tgg ggc atg ggt gat		691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp		
	185 190 195	
ttc aat gat tta gga aac ttg gca agt gtg gtt gcc cag gat gga gca		739
Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala		
	200 205 210	
gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct		787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro		
	215 220 225	

act	gag	gac	tct	cct	tat	ctg	ccc	aca	acc	agg	cgc	ttt	atc	aac	ccg	835
Thr	Glu	Asp	Ser	Pro	Tyr	Leu	Pro	Thr	Thr	Arg	Arg	Phe	Ile	Asn	Pro	
230					235					240					245	
atc	tac	att	cgg	gta	gaa	gat	att	ccg	gag	ttt	aat	cag	ctt	gag	att	883
Ile	Tyr	Ile	Arg	Val	Glu	Asp	Ile	Pro	Glu	Phe	Asn	Gln	Leu	Glu	Ile	
				250					255					260		
gat	cta	cgc	gat	gat	atc	gca	gag	atg	gct	gcg	gaa	ttc	cgc	gaa	cgc	931
Asp	Leu	Arg	Asp	Asp	Ile	Ala	Glu	Met	Ala	Ala	Glu	Phe	Arg	Glu	Arg	
			265					270					275			
aat	ctg	acc	tca	gac	atc	att	gag	cgc	aat	gac	gtc	tac	gct	gca	aag	979
Asn	Leu	Thr	Ser	Asp	Ile	Ile	Glu	Arg	Asn	Asp	Val	Tyr	Ala	Ala	Lys	
		280					285					290				
ctt	caa	gtg	ctg	cgc	gcc	att	ttt	gaa	atg	cct	cgt	tcc	agc	gaa	cgt	1027
Leu	Gln	Val	Leu	Arg	Ala	Ile	Phe	Glu	Met	Pro	Arg	Ser	Ser	Glu	Arg	
	295					300					305					
gaa	gcc	aac	ttt	gtc	tcc	ttc	gtg	caa	cgg	gaa	ggc	caa	ggg	ctt	att	1075
Glu	Ala	Asn	Phe	Val	Ser	Phe	Val	Gln	Arg	Glu	Gly	Gln	Gly	Leu	Ile	
310					315					320				325		
gat	ttc	gcc	acc	tgg	tgc	gcg	gac	cgc	gaa	act	gca	cag	tct	gaa	tct	1123
Asp	Phe	Ala	Thr	Trp	Cys	Ala	Asp	Arg	Glu	Thr	Ala	Gln	Ser	Glu	Ser	
				330				335						340		
gtc	cac	gga	act	gag	cca	gac	cgc	gat	gag	ctg	acc	atg	ttc	tac	atg	1171
Val	His	Gly	Thr	Glu	Pro	Asp	Arg	Asp	Glu	Leu	Thr	Met	Phe	Tyr	Met	
			345					350					355			
tgg	ttg	cag	tgg	cta	tgt	gat	gag	cag	ctg	gcg	gca	gct	caa	aag	cgc	1219
Trp	Leu	Gln	Trp	Leu	Cys	Asp	Glu	Gln	Leu	Ala	Ala	Ala	Gln	Lys	Arg	
		360					365					370				
gct	gtc	gat	gcc	gga	atg	tcg	atc	ggc	atc	atg	gca	gac	ctg	gca	gtt	1267
Ala	Val	Asp	Ala	Gly	Met	Ser	Ile	Gly	Ile	Met	Ala	Asp	Leu	Ala	Val	
	375					380					385					
ggg	gtg	cat	cca	ggg	ggg	gct	gat	gcc	cag	aac	ctc	agc	cac	gta	ctt	1315
Gly	Val	His	Pro	Gly	Gly	Ala	Asp	Ala	Gln	Asn	Leu	Ser	His	Val	Leu	
390				395					400					405		
gct	ccg	gat	gcg	tca	gtg	ggc	gcc	cca	cca	gat	gga	tac	aac	cag	cag	1363
Ala	Pro	Asp	Ala	Ser	Val	Gly	Ala	Pro	Pro	Asp	Gly	Tyr	Asn	Gln	Gln	
				410				415						420		
ggc	caa	gac	tgg	tcc	cag	cca	cca	tgg	cat	cca	gtg	cgt	ctt	gca	gag	1411
Gly	Gln	Asp	Trp	Ser	Gln	Pro	Pro	Trp	His	Pro	Val	Arg	Leu	Ala	Glu	
			425					430					435			
gaa	ggc	tac	att	ccg	tgg	cgt	aat	ctg	ctg	cgc	act	gtg	ctg	cgt	cac	1459
Glu	Gly	Tyr	Ile	Pro	Trp	Arg	Asn	Leu	Leu	Arg	Thr	Val	Leu	Arg	His	
		440					445					450				
tcc	ggc	gga	atc	cgc	gtg	gac	cac	gtt	ctt	ggg	ttg	ttc	agg	ctc	ttt	1507
Ser	Gly	Gly	Ile	Arg	Val	Asp	His	Val	Leu	Gly	Leu	Phe	Arg	Leu	Phe	
	455					460					465					
gtc	atg	cca	cgc	atg	caa	tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	1555

Val 470	Met	Pro	Arg	Met	Gln 475	Ser	Pro	Ala	Thr	Gly 480	Thr	Tyr	Ile	Arg	Phe 485	
gac	cat	aat	gcg	ttg	gta	ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	1603
Asp	His	Asn	Ala	Leu	Val	Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	
				490					495					500		
ggc	gcc	gtt	gtc	att	ggg	gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	1651
Gly	Ala	Val	Val	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	
				505				510					515			
caa	gat	gca	ttg	gct	cag	cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	1699
Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	
		520					525					530				
ttc	gag	cat	tcc	cca	agc	cag	ccg	ggg	cct	cgc	cgc	cag	gaa	gag	tat	1747
Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	
	535					540					545					
cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	
550					555					560					565	
gct	ggg	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu	Glu	Gly	Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	
				570					575					580		
gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891
Val	Leu	Asn	Thr	Asp	Pro	Ala	Ala	Glu	Leu	Ala	Glu	Asp	Leu	Gln	Trp	
			585					590					595			
caa	gcg	gag	atc	ctt	gat	gtc	gca	gca	tct	gcc	aac	gca	ttg	cca	gcc	1939
Gln	Ala	Glu	Ile	Leu	Asp	Val	Ala	Ala	Ser	Ala	Asn	Ala	Leu	Pro	Ala	
		600					605					610				
cgg	gaa	tac	gtg	gga	ctc	gaa	cgc	gat	cag	cgc	ggg	gag	ttg	gct	gag	1987
Arg	Glu	Tyr	Val	Gly	Leu	Glu	Arg	Asp	Gln	Arg	Gly	Glu	Leu	Ala	Glu	
	615					620					625					
ctg	ttg	gaa	ggc	ctg	cac	act	ttc	gtt	gcg	aaa	acc	cct	tca	gca	ctg	2035
Leu	Leu	Glu	Gly	Leu	His	Thr	Phe	Val	Ala	Lys	Thr	Pro	Ser	Ala	Leu	
630					635					640				645		
acc	tgt	gtc	tgc	ttg	gta	gac	atg	gtc	ggg	gaa	aag	cgg	gca	cag	aat	2083
Thr	Cys	Val	Cys	Leu	Val	Asp	Met	Val	Gly	Glu	Lys	Arg	Ala	Gln	Asn	
				650					655					660		
cag	ccg	ggc	aca	acg	agg	gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	2131
Gln	Pro	Gly	Thr	Thr	Arg	Asp	Met	Tyr	Pro	Asn	Trp	Cys	Ile	Pro	Leu	
			665				670						675			
tgt	gac	agc	gaa	ggc	aac	tcc	gtg	ctc	att	gaa	tcg	ctg	cgt	gaa	aat	2179
Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	
		680					685					690				
gag	ctg	tat	cac	cgt	gtg	gca	aag	gca	agc	aag	cga	gat	taggtccgct			2228
Glu	Leu	Tyr	His	Arg	Val	Ala	Lys	Ala	Ser	Lys	Arg	Asp				
	695					700					705					
tcagttgtgg	tgg															2241

<210> 410
 <211> 706
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 410

```

Val Thr Ala Arg Arg Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val
 1           5           10           15

Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp
          20           25           30

Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr
          35           40           45

Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe
          50           55           60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val
          65           70           75           80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro
          85           90           95

Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser
          100          105          110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp
          115          120          125

Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His
          130          135          140

Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile
          145          150          155          160

Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro
          165          170          175

Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser
          180          185          190

Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val
          195          200          205

Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala
          210          215          220

Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg
          225          230          235          240

Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe
          245          250          255

Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala
          260          265          270

Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp
          275          280          285

```

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro
 290 295 300
 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu
 305 310 315 320
 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr
 325 330 335
 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu
 340 345 350
 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala
 355 360 365
 Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met
 370 375 380
 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn
 385 390 395 400
 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp
 405 410 415
 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro
 420 425 430
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg
 435 440 445
 Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly
 450 455 460
 Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly
 465 470 475 480
 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu
 485 490 495
 Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr
 500 505 510
 Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly
 515 520 525
 Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg
 530 535 540
 Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His
 545 550 555 560
 Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu
 565 570 575
 Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala
 580 585 590
 Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala
 595 600 605
 Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg

610	615	620
Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys		
625	630	635 640
Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu		
	645	650 655
Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn		
	660	665 670
Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu		
	675	680 685
Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys		
	690	695 700
Arg Asp		
705		

<210> 411
 <211> 2223
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2200)
 <223> FRXA00879

<400> 411
 aaaagatgta ttttctaaca aacttacocct cacgctacaa atatgctgtg cccacacgct 60
 attagtggca taatgtttgtg ttgtgactgc togcagattt ttg aat gaa ctc gcc 115
 Leu Asn Glu Leu Ala
 1 5
 gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163
 Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His
 10 15 20
 att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt 211
 Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly
 25 30 35
 gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259
 Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg
 40 45 50
 caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca 307
 Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro
 55 60 65
 tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355
 Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val
 70 75 80 85
 cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg 403
 His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr
 90 95 100

cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att	451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile	
105 110 115	
gat ggg att agg tgg ggc gag gca tcg ttt aag att cct ggt gat ctc	499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu	
120 125 130	
ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct	547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala	
135 140 145	
gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag	595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys	
150 155 160 165	
tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg	643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val	
170 175 180	
cgt tcc acg ttg tgg ggc atg ggt gat ttc aat gat tta gga aac	691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn	
185 190 195	
ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac	739
Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn	
200 205 210	
ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat	787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
215 220 225	
ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa	835
Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu	
230 235 240 245	
gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc	883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile	
250 255 260	
gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc	931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile	
265 270 275	
att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc	979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala	
280 285 290	
att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc	1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
295 300 305	
ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc	1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys	
310 315 320 325	
gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca	1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro	
330 335 340	

gac	cgc	gat	gag	ctg	acc	atg	ttc	tac	atg	tgg	ttg	cag	tgg	cta	tgt	1171
Asp	Arg	Asp	Glu	Leu	Thr	Met	Phe	Tyr	Met	Trp	Leu	Gln	Trp	Leu	Cys	
			345					350					355			
gat	gag	cag	ctg	gcg	gca	gct	caa	aag	cgc	gct	gtc	gat	gcc	gga	atg	1219
Asp	Glu	Gln	Leu	Ala	Ala	Ala	Gln	Lys	Arg	Ala	Val	Asp	Ala	Gly	Met	
		360					365					370				
tcg	atc	ggc	atc	atg	gca	gac	ctg	gca	gtt	ggg	gtg	cat	cca	ggg	ggg	1267
Ser	Ile	Gly	Ile	Met	Ala	Asp	Leu	Ala	Val	Gly	Val	His	Pro	Gly	Gly	
	375					380					385					
gct	gat	gcc	cag	aac	ctc	agc	cac	gta	ctt	gct	ccg	gat	gcg	tca	gtg	1315
Ala	Asp	Ala	Gln	Asn	Leu	Ser	His	Val	Leu	Ala	Pro	Asp	Ala	Ser	Val	
390					395					400					405	
ggc	gcc	cca	cca	gat	gga	tac	aac	cag	cag	ggc	caa	gac	tgg	tcc	cag	1363
Gly	Ala	Pro	Pro	Asp	Gly	Tyr	Asn	Gln	Gln	Gly	Gln	Asp	Trp	Ser	Gln	
				410				415						420		
cca	cca	tgg	cat	cca	gtg	cgt	ctt	gca	gag	gaa	ggc	tac	att	ccg	tgg	1411
Pro	Pro	Trp	His	Pro	Val	Arg	Leu	Ala	Glu	Glu	Gly	Tyr	Ile	Pro	Trp	
			425					430					435			
cgt	aat	ctg	ctg	cgc	act	gtg	ctg	cgt	cac	tcc	ggc	gga	atc	cgc	gtg	1459
Arg	Asn	Leu	Leu	Arg	Thr	Val	Leu	Arg	His	Ser	Gly	Gly	Ile	Arg	Val	
		440					445					450				
gac	cac	gtt	ctt	ggg	ttg	ttc	agg	ctc	ttt	gtc	atg	cca	cgc	atg	caa	1507
Asp	His	Val	Leu	Gly	Leu	Phe	Arg	Leu	Phe	Val	Met	Pro	Arg	Met	Gln	
	455					460					465					
tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	gac	cat	aat	gcg	ttg	gta	1555
Ser	Pro	Ala	Thr	Gly	Thr	Tyr	Ile	Arg	Phe	Asp	His	Asn	Ala	Leu	Val	
470					475					480					485	
ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	ggc	gcc	gtt	gtc	att	ggg	1603
Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Gly	Ala	Val	Val	Ile	Gly	
				490					495					500		
gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	caa	gat	gca	ttg	gct	cag	1651
Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	Gln	Asp	Ala	Leu	Ala	Gln	
		505						510					515			
cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	ttc	gag	cat	tcc	cca	agc	1699
Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	Phe	Glu	His	Ser	Pro	Ser	
		520					525					530				
cag	ccg	ggg	cct	cgc	cgc	cag	gaa	gag	tat	cgt	ccg	ctg	gcc	ttg	acc	1747
Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	Arg	Pro	Leu	Ala	Leu	Thr	
	535					540					545					
act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	gct	ggg	tat	ttg	gag	ggc	1795
Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	Ala	Gly	Tyr	Leu	Glu	Gly	
550					555					560					565	
gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	gtg	ctc	aac	act	gat	cct	1843
Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	Val	Leu	Asn	Thr	Asp	Pro	
				570					575					580		
gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	caa	gcg	gag	atc	ctt	gat	1891

Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp
 585 590 595

gtc gca gca tct gcc aac gca ttg cca gcc cgg gaa tac gtg gga ctc 1939
 Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu
 600 605 610

gaa cgc gat cag cgc ggt gag ttg gct gag ctg ttg gaa ggc ctg cac 1987
 Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His
 615 620 625

act ttc gtt gcg aaa acc cct tca gca ctg acc tgt gtc tgc ttg gta 2035
 Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val
 630 635 640 645

gac atg gtc ggt gaa aag cgg gca cag aat cag ccg ggc aca acg agg 2083
 Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg
 650 655 660

gat atg tat ccc aac tgg tgt atc cca ctg tgt gac agc gaa ggc aac 2131
 Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn
 665 670 675

tcc gtg ctc att gaa tcg ctg cgt gaa aat gag ctg tat cac cgt gtg 2179
 Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val
 680 685 690

gca aag gca agc aag cga gat taggtccgct tcagttgtgg tgg 2223
 Ala Lys Ala Ser Lys Arg Asp
 695 700

<210> 412

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp
 1 5 10 15

Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile
 20 25 30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp
 35 40 45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr
 50 55 60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val
 65 70 75 80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu
 85 90 95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr
 100 105 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys
 115 120 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser
 130 135 140
 Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu
 145 150 155 160
 Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala
 165 170 175
 Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe
 180 185 190
 Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp
 195 200 205
 Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr
 210 215 220
 Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile
 225 230 235 240
 Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp
 245 250 255
 Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn
 260 265 270
 Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu
 275 280 285
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu
 290 295 300
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp
 305 310 315 320
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val
 325 330 335
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp
 340 345 350
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala
 355 360 365
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly
 370 375 380
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala
 385 390 395 400
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly
 405 410 415
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu
 420 425 430
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser
 435 440 445

Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val
 450 455 460
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp
 465 470 475 480
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly
 485 490 495
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln
 500 505 510
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe
 515 520 525
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg
 530 535 540
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala
 545 550 555 560
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val
 565 570 575
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln
 580 585 590
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg
 595 600 605
 Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu
 610 615 620
 Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr
 625 630 635 640
 Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln
 645 650 655
 Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys
 660 665 670
 Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu
 675 680 685
 Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp
 690 695 700

<210> 413

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN00043

<400> 413

aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60

gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg	115
Met Ala Glu Val Val	
1 5	
cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga	163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg	
10 15 20	
att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac	211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn	
25 30 35	
ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga	259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly	
40 45 50	
ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat	307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His	
55 60 65	
aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag	355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln	
70 75 80 85	
gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met	
90 95 100	
ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835
 Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
 230 235 240 245
 ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883
 Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
 250 255 260
 gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931
 Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
 265 270 275
 aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979
 Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
 280 285 290
 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
 295 300 305
 gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
 310 315 320 325
 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
 330 335 340
 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
 345 350 355
 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
 360 365 370
 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
 375 380 385
 taaatacagag caaaactttc ctg 1287

<210> 414

<211> 388

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 414

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
 1 5 10 15
 Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
 20 25 30
 Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
 35 40 45
 Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65 70 75 80
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
 85 90 95
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100 105 110
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115 120 125
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
 130 135 140
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
 145 150 155 160
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
 165 170 175
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
 180 185 190
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
 195 200 205
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
 210 215 220
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
 225 230 235 240
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
 245 250 255
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
 260 265 270
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
 275 280 285
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
 290 295 300
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly
 305 310 315 320
 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly
 325 330 335
 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys
 340 345 350
 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn
 355 360 365
 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp
 370 375 380
 His Gln Val Ile

```
<210> 415
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1264)
<223> FRXA00043
```

599

Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	
gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc	1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser	
345 350 355	
gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac	1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp	
360 365 370	
tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att	1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile	
375 380 385	
taaatacgag caaaactttc ctg	1287

<210> 416

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

```

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
 1              5              10              15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
      20              25              30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
      35              40              45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
      50              55              60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
      65              70              75              80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
      85              90              95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
      100              105              110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
      115              120              125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
      130              135              140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
      145              150              155              160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
      165              170              175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
      180              185              190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
      195              200              205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
      210              215              220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
      225              230              235              240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
      245              250              255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
      260              265              270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
      275              280              285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
      290              295              300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

```

[illegible]

```
<210> 417
<211> 1584
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1561)
<223> RXN01752
```

<400> 417															
gaaatgacgt gaccatogat accaataccc aattgaaaga tcttgacctg gtcagccaag															60
ttggccgtca gatcgtggca gaacaacagg tggggagggtc atg atg gaa caa gat															115
Met Met Glu Gln Asp															
1 5															
ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa															163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys															
10 15 20															
aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg															211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro															
25 30 35															
cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc															259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe															
40 45 50															
att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa															307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln															
55 60 65															
gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att															355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile															
70 75 80 85															
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa															403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu															
90 95 100															
tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac															451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp															

105	110	115	
aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag			499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu			
120	125	130	
gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag			547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys			
135	140	145	
cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg			595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr			
150	155	160	165
atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att			643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile			
170	175	180	
aag gtg ccg cca gcg cag ccc cgc acc aag ccg aag gcc tgt aac tat			691
Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr			
185	190	195	
gga ttg cac ttt gcc acg ggg gaa att gtc acg atc ttt gac gcg gaa			739
Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu			
200	205	210	
gac atg cca gat ccc ctc caa ctg cgt cgc gtg gtg gtg gca ttt gaa			787
Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val Val Val Ala Phe Glu			
215	220	225	
cgc tcg gct tcc aat acg gtg tgc gtc cag tca agg ttg tcg tat cga			835
Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser Arg Leu Ser Tyr Arg			
230	235	240	245
aac gcc agg cag aat ctg cta act gcg tgg ttc acc att gaa tat gac			883
Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp			
250	255	260	
gtg tgg ttt aac ttc ctg ctg cca ggc gtc atg cgc atg aac gca cct			931
Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met Arg Met Asn Ala Pro			
265	270	275	
gtc cca ttg ggc ggt acc tcc aac cat ctg ctc acg ggt gtc ctg aaa			979
Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys			
280	285	290	
gat ctc ggc gcg tgg gat cct ttc aat gtc aca gaa aat gcc gac ctc			1027
Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu			
295	300	305	
ggc gta ccc atc gcg gca aaa gga tat tcc acc gcg gtg ttg gat tcg			1075
Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser			
310	315	320	325
gtg acg tgg gag gaa gca aac tcc gac acc atc aac tgg ttg cgc cag			1123
Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln			
330	335	340	
cgt tct cgc tgg tac aag ggc tat ctg caa aca tgg ctt gtg tat atg			1171
Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met			
345	350	355	

cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg 1219
 Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val
 360 365 370

cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat 1267
 Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn
 375 380 385

ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc 1315
 Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly
 390 395 400 405

acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg 1363
 Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val
 410 415 420

tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc 1411
 Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly
 425 430 435

tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc 1459
 Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe
 440 445 450

ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg 1507
 Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp
 455 460 465

caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555
 Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu
 470 475 480 485

gag gcg taagcgggtgc ccatcgtcaa acc 1584
 Glu Ala

<210> 418

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala
 1 5 10 15

Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
 20 25 30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
 35 40 45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
 50 55 60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65 70 75 80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
 100 105 110
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
 115 120 125
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
 130 135 140
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
 145 150 155 160
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
 165 170 175
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro
 180 185 190
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr
 195 200 205
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val
 210 215 220
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser
 225 230 235 240
 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe
 245 250 255
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met
 260 265 270
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu
 275 280 285
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr
 290 295 300
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr
 305 310 315 320
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile
 325 330 335
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr
 340 345 350
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly
 355 360 365
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile
 370 375 380
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile
 385 390 395 400
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe
 420 425 430
 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile
 435 440 445
 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala
 450 455 460
 Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys
 465 470 475 480
 Thr Ala His Gly Leu Glu Ala
 485

<210> 419

<211> 689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (19)..(666)

<223> FRXA01839

<400> 419

ttctgtctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt 51
 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly
 1 5 10
 acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99
 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp
 15 20 25
 gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala
 30 35 40
 gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu
 45 50 55
 gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr
 60 65 70 75
 aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp
 80 85 90
 tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu
 95 100 105
 atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr
 110 115 120
 ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435
 Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125	130	135	
ttc cca cct gcg gtg tac	tac cca gcg ttg gtg	tgt ttg gtg gcc	483
Phe Pro Pro Ala Val Tyr	Tyr Pro Ala Leu Val Cys	Leu Val Val Ala	
140	145	150 155	
aat gct gcg acc atc ttt atg	aat ctc att ggc tgc	cgg gaa ggc cgc	531
Asn Ala Ala Thr Ile Phe	Met Asn Leu Ile Gly Cys	Arg Glu Gly Arg	
160	165	170	
gac ccc ttg ctg ctc atc gcg	gtt ctc acg ttc ccg	ctg tat tgg ctg	579
Asp Pro Leu Leu Ile Ala	Val Leu Thr Phe Pro	Leu Tyr Trp Leu	
175	180	185	
ctc atg agc att gca gcg ttg	aaa ggc acg tgg caa	ttg atc acg cga	627
Leu Met Ser Ile Ala Ala	Leu Lys Gly Thr Trp	Gln Leu Ile Thr Arg	
190	195	200	
cca tcc tat tgg gag aaa act	gcc cac gga ttg gag	gcg taagcgggtgc	676
Pro Ser Tyr Trp Glu Lys	Thr Ala His Gly Leu	Glu Ala	
205	210	215	
ccatcgtcaa acc			689
<210> 420			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 420			
Met Arg Met Asn Ala Pro	Val Pro Leu Gly Gly Thr	Ser Asn His Leu	
1	5	10 15	
Leu Thr Gly Val Leu Lys	Asp Leu Gly Ala Trp	Asp Pro Phe Asn Val	
20	25	30	
Thr Glu Asp Ala Asp Leu	Gly Val Arg Ile Ala	Ala Lys Gly Tyr Ser	
35	40	45	
Thr Ala Val Leu Asp Ser	Val Thr Trp Glu Glu	Ala Asn Ser Asp Thr	
50	55	60	
Ile Asn Trp Leu Arg Gln	Arg Ser Arg Trp Tyr	Lys Gly Tyr Leu Gln	
65	70	75 80	
Thr Trp Leu Val Tyr Met	Arg Arg Pro Lys Trp	Leu Val Gln Glu Leu	
85	90	95	
Gly Ile Ile Pro Ala Val	Arg Phe Thr Phe Leu	Met Ala Gly Thr Pro	
100	105	110	
Ile Ile Ala Val Leu Asn	Leu Leu Phe Trp Tyr	Leu Ser Leu Thr Trp	
115	120	125	
Ile Leu Gly Gln Pro Gly	Thr Ile Glu Gln Met	Phe Pro Pro Ala Val	
130	135	140	
Tyr Tyr Pro Ala Leu Val	Cys Leu Val Val Ala	Asn Ala Ala Thr Ile	
145	150	155 160	

Phe	Met	Asn	Leu	Ile	Gly	Cys	Arg	Glu	Gly	Arg	Asp	Pro	Leu	Leu	Leu
				165					170					175	
Ile	Ala	Val	Leu	Thr	Phe	Pro	Leu	Tyr	Trp	Leu	Leu	Met	Ser	Ile	Ala
			180					185					190		
Ala	Leu	Lys	Gly	Thr	Trp	Gln	Leu	Ile	Thr	Arg	Pro	Ser	Tyr	Trp	Glu
		195					200					205			
Lys	Thr	Ala	His	Gly	Leu	Glu	Ala								
	210					215									

```
<210> 421
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1027)
<223> RXA01859
```

<400> 421																
tacgcccagg	gtttccatat	tggtaaattct	aagccgattg	atgaattttat	agctacttat	60										
ctcgagacga	accaaaccgc	tacctggggg	taggaagaat	atg	aaa	aag	aag	agc	115							
				Met	Lys	Lys	Lys	Ser								
				1				5								
ttt	cca	atc	gca	aga	gtc	atc	ggt	atc	ggc	gtc	ctt	ggc	atc	gcc	ggg	163
Phe	Pro	Ile	Ala	Arg	Val	Ile	Gly	Ile	Gly	Val	Leu	Gly	Ile	Ala	Gly	
				10					15					20		
atg	gga	ata	ttg	ttg	cta	tgg	ctt	gca	gtt	acc	ctg	tct	gat	cca	gca	211
Met	Gly	Ile	Leu	Leu	Leu	Trp	Leu	Ala	Val	Thr	Leu	Ser	Asp	Pro	Ala	
			25					30					35			
tca	ccg	ggt	gcc	aaa	gaa	acc	gaa	gtc	ttt	gat	agg	tgg	aaa	gtg	ctc	259
Ser	Pro	Gly	Ala	Lys	Glu	Thr	Glu	Val	Phe	Asp	Arg	Trp	Lys	Val	Leu	
		40					45					50				
ttt	gat	gac	tat	att	cca	cca	gtc	agg	gta	ttg	gtt	gct	gcg	att	atc	307
Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu	Val	Ala	Ala	Ile	Ile	
	55					60					65					
gtt	gca	tta	att	ttc	gtc	ttt	atc	gct	gcc	aca	gtg	gaa	cga	acc	gta	355
Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr	Val	Glu	Arg	Thr	Val	
	70				75				80						85	
acc	aac	cgc	tac	cga	agc	tcc	gta	gac	ggc	gaa	aga	gtg	cca	tta	gcg	403
Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu	Arg	Val	Pro	Leu	Ala	
				90					95					100		
ccg	aag	att	gtg	atg	gca	gaa	acc	cga	ggg	gta	ttt	cat	gga	ccg	att	451
Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val	Phe	His	Gly	Pro	Ile	
			105					110					115			
acc	att	aac	gtg	ctc	gtg	cca	gca	cac	aat	gag	gcg	gaa	aga	att	act	499
Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu	Ala	Glu	Arg	Ile	Thr	
		120					125					130				

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc 547
 Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile
 135 140 145
 gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt 595
 Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg
 150 155 160 165
 gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag 643
 Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys
 170 175 180
 gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg 691
 Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly
 185 190 195
 gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa 739
 Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln
 200 205 210
 ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta 787
 Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu
 215 220 225
 atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt 835
 Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu
 230 235 240 245
 ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr
 250 255 260
 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe
 265 270 275
 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile
 280 285 290
 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg
 295 300 305
 taatgagttg accctggcctt tga 1050

<210> 422

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Met Lys Lys Lys Ser Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val
 1 5 10 15

Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr
 20 25 30

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp

35					40					45						
Arg	Trp	Lys	Val	Leu	Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu	
50					55					60						
Val	Ala	Ala	Ile	Ile	Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr	
65					70					75					80	
Val	Glu	Arg	Thr	Val	Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu	
85					90					95						
Arg	Val	Pro	Leu	Ala	Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val	
100					105					110						
Phe	His	Gly	Pro	Ile	Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu	
115					120					125						
Ala	Glu	Arg	Ile	Thr	Gly	Thr	Ile	Gln	Ala	Leu	Lys	Ser	Gln	His	Glu	
130					135					140						
Pro	Pro	Glu	Arg	Ile	Val	Val	Val	Ala	Asp	Asn	Cys	Thr	Asp	Glu	Thr	
145					150					155					160	
Thr	Glu	Leu	Ala	Arg	Ala	Glu	Gly	Val	Glu	Val	Leu	Glu	Thr	Val	Asn	
165					170					175						
Asn	Lys	Phe	Lys	Lys	Ala	Gly	Gly	Leu	Asn	Gln	Ala	Leu	Ser	Arg	Met	
180					185					190						
Leu	Pro	Thr	Leu	Gly	Glu	Asn	Asp	Ile	Val	Met	Ile	Val	Asp	Ala	Asp	
195					200					205						
Thr	Ala	Leu	Asp	Gln	Gly	Phe	Leu	Lys	Glu	Ala	Arg	Arg	Arg	Phe	Glu	
210					215					220						
Ser	Asp	Arg	Ala	Leu	Met	Ala	Val	Gly	Gly	Leu	Phe	Tyr	Gly	Glu	Ser	
225					230					235					240	
Gly	Ser	Gly	Trp	Leu	Gly	Gln	Tyr	Gln	Arg	Asn	Glu	Tyr	Thr	Arg	Tyr	
245					250					255						
Ser	Arg	Asp	Ile	Tyr	Arg	Arg	Arg	Gly	Arg	Val	Phe	Val	Leu	Thr	Gly	
260					265					270						
Thr	Ala	Ser	Ala	Phe	Arg	Pro	Arg	Gly	Leu	Arg	Thr	Val	Ala	Glu	Ser	
275					280					285						
Arg	Gly	Thr	Leu	Ile	Pro	Gly	Arg	Lys	Ala	Asp	Val	Tyr	Asp	Thr	Ala	
290					295					300						
Gly	Val	Asp	Arg	Arg												
305																

<210> 423

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA00042

<400> 423

```

gtggtctttg actcaaacgg ccagttacaa caggtccatt tagaccatca agtaatttaa 60
atacgagcaa aactttcctg ataataaaag gagtccgacc atg gac atc atc atc 115
                                         Met Asp Ile Ile Ile
                                         1           5

tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Ala Leu Ile Ala
              10              15              20

ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tgc tca 211
Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
              25              30              35

cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
              40              45              50

gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
              55              60              65

tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu
              70              75              80              85

ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat 403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp
              90              95              100

ggg gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag 451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys
              105              110              115

atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac 499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn
              120              125              130

ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca 547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr
              135              140              145

aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc 595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe
              150              155              160              165

ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg 643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu
              170              175              180

ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa 691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu
              185              190              195

gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc 739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala
              200              205              210

```

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile
 215 220 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg
 230 235 240 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882
 Leu Met Glu Gln Leu Lys Leu Arg
 250

<210> 424

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala
 1 5 10 15

Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu
 20 25 30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met
 35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu
 50 55 60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys
 65 70 75 80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu
 85 90 95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala
 100 105 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu
 115 120 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser
 130 135 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu
 145 150 155 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala
 165 170 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu
 180 185 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu
 195 200 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn
 210 215 220

Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn
225 230 235 240

Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg
245 250

<210> 425

<211> 1998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1975)

<223> RXA01482

<400> 425

ttgctgtgctg caacttaatt atggctcctcc cagctcagtg tgctgtgtgg attgtttatt 60

ctcgtccatt aagtgatcga. gaaaaagttg ttgtaaagtc atg cgc atg tgt gga 115
Met Arg Met Cys Gly
1 5

att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163
Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala
10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat 211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr
25 30 35

gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga 259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg
40 45 50

aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca 307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala
55 60 65

cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act 355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr
70 75 80 85

cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat 403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn
90 95 100

ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa 451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu
105 110 115

ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc 499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr
120 125 130

gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag 547
Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln
135 140 145

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	
ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315

Gly 390	Ser	Thr	Leu	Pro	Arg 395	Glu	Ala	Asp	Ala	Ser 400	Leu	Tyr	Thr	Tyr	Ala 405	
ggc	cct	gag	atc	gct	gtg	gcg	tcc	acc	aag	gcg	ttc	ttg	gct	cag	atc	1363
Gly	Pro	Glu	Ile	Ala	Val	Ala	Ser	Thr	Lys	Ala	Phe	Leu	Ala	Gln	Ile	
				410					415					420		
act	gct	tct	tac	ttg	ctt	ggc	ctg	tac	ttg	gct	cag	ctg	cgc	ggc	aac	1411
Thr	Ala	Ser	Tyr	Leu	Leu	Gly	Leu	Tyr	Leu	Ala	Gln	Leu	Arg	Gly	Asn	
			425					430					435			
aag	ttc	gct	gat	gag	gtt	tct	tcc	att	ctg	gac	agc	ctg	cgt	gag	atg	1459
Lys	Phe	Ala	Asp	Glu	Val	Ser	Ser	Ile	Leu	Asp	Ser	Leu	Arg	Glu	Met	
		440					445					450				
cct	gag	aag	att	cag	cag	gtc	atc	gat	gca	gaa	gag	cag	atc	aag	aag	1507
Pro	Glu	Lys	Ile	Gln	Gln	Val	Ile	Asp	Ala	Glu	Glu	Gln	Ile	Lys	Lys	
	455					460					465					
ctt	ggc	caa	gat	atg	gca	gat	gct	aag	tct	gtg	ctg	ttc	ctg	ggc	cgc	1555
Leu	Gly	Gln	Asp	Met	Ala	Asp	Ala	Lys	Ser	Val	Leu	Phe	Leu	Gly	Arg	
470					475					480					485	
cac	gtt	ggt	ttc	cca	gtt	gcg	ctt	gag	ggt	gcg	ttg	aag	ctc	aag	gag	1603
His	Val	Gly	Phe	Pro	Val	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu	
				490					495					500		
atc	gca	tac	ctg	cac	gct	gaa	ggt	ttc	gct	gca	ggc	gag	ctc	aag	cac	1651
Ile	Ala	Tyr	Leu	His	Ala	Glu	Gly	Phe	Ala	Ala	Gly	Glu	Leu	Lys	His	
			505					510					515			
ggc	cca	att	gct	ttg	gtt	gag	gaa	ggc	cag	ccg	atc	ttc	gtt	atc	gtg	1699
Gly	Pro	Ile	Ala	Leu	Val	Glu	Glu	Gly	Gln	Pro	Ile	Phe	Val	Ile	Val	
		520				525						530				
cct	tca	cct	cgt	ggt	cgc	gat	tcc	ctg	cac	tcc	aag	gtt	gtc	tcc	aac	1747
Pro	Ser	Pro	Arg	Gly	Arg	Asp	Ser	Leu	His	Ser	Lys	Val	Val	Ser	Asn	
	535					540					545					
att	cag	gag	atc	cgt	gca	cgt	ggc	gct	gtc	acc	atc	gtg	att	gca	gag	1795
Ile	Gln	Glu	Ile	Arg	Ala	Arg	Gly	Ala	Val	Thr	Ile	Val	Ile	Ala	Glu	
550					555					560				565		
gaa	ggc	gat	gag	gct	gtc	aac	gat	tac	gcc	aac	ttc	atc	atc	cgc	att	1843
Glu	Gly	Asp	Glu	Ala	Val	Asn	Asp	Tyr	Ala	Asn	Phe	Ile	Ile	Arg	Ile	
				570					575					580		
cct	cag	gcc	cca	acc	ctg	atg	cag	cct	ctg	ctg	tcc	acc	gtg	cct	ctg	1891
Pro	Gln	Ala	Pro	Thr	Leu	Met	Gln	Pro	Leu	Leu	Ser	Thr	Val	Pro	Leu	
			585					590					595			
cag	atc	ttt	gcg	tgc	gct	gtg	gca	acc	gca	aag	ggc	tac	aac	gtg	gat	1939
Gln	Ile	Phe	Ala	Cys	Ala	Val	Ala	Thr	Ala	Lys	Gly	Tyr	Asn	Val	Asp	
		600					605					610				
cag	cct	cgt	aac	ctg	gca	aag	tct	gtc	acc	gtc	gaa	taaaaagatt				1985
Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu					
	615					620					625					
tcgcttctcg	acg															1998

<210> 426
 <211> 625
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 426

```

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser
 1           5           10           15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu
      20           25           30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
      35           40           45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
      50           55           60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
      65           70           75           80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro
      85           90           95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile
      100          105          110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn
      115          120          125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu
      130          135          140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu
      145          150          155          160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala
      165          170          175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val
      180          185          190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
      195          200          205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val
      210          215          220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser
      225          230          235          240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala
      245          250          255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln
      260          265          270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly
      275          280          285

```

Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser
 290 295 300
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly
 305 310 315 320
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu
 325 330 335
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu
 340 345 350
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr
 355 360 365
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala
 370 375 380
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser
 385 390 395 400
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala
 405 410 415
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala
 420 425 430
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp
 435 440 445
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu
 450 455 460
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val
 465 470 475 480
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala
 485 490 495
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala
 500 505 510
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro
 515 520 525
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser
 530 535 540
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr
 545 550 555 560
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn
 565 570 575
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu
 580 585 590
 Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys
 595 600 605
 Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val

610 615 620

Glu
625

<210> 427
<211> 666
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(666)
<223> RXN03179

<400> 427

gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca	48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	
gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga	192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg	
50 55 60	
cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc	240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr	
65 70 75 80	
gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat	288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp	
85 90 95	
cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac	336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr	
100 105 110	
acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc	384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile	
115 120 125	
gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca	432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala	
130 135 140	
atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg	480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala	
145 150 155 160	
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat	528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp	
165 170 175	

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666
 Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 429
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(672)
 <223> FRXA02872

<400> 429
 gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca 48
 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96
 Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 431

<211> 533
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(510)
 <223> RXN03180

<400> 431

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg	48
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp	
1 5 10 15	
ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca	96
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala	
20 25 30	
gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc	144
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg	
35 40 45	
gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac	192
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn	
50 55 60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc	240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe	
65 70 75 80	
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga	288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly	
85 90 95	
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc	336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu	
100 105 110	
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat	384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp	
115 120 125	
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa	432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln	
130 135 140	
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac	480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His	
145 150 155 160	
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga	530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln	
165 170	
tgt	533

<210> 432
 <211> 170
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95
 Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170

<210> 433

<211> 533

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(510)

<223> FRXA02873

<400> 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn

50	55	60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc			240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
65	70	75	80
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga			288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
	85	90	95
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc			336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
	100	105	110
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat			384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			
	115	120	125
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa			432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln			
	130	135	140
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac			480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His			
	145	150	155
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga			530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln			
	165	170	
tgt			533

<210> 434

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp

115	120	125
Glu Asn Tyr Asp Leu Val	Ile Asn Thr Gly Ser Met	Thr Tyr Glu Gln
130	135	140
Ile Val Asp Leu Val Val	Glu Thr Tyr Ala Arg Lys	Tyr Pro Leu His
145	150	155
Val Arg Ile Ile Pro Asn	Gly Lys Asp Gln	
165	170	

<210> 435

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA02292

<400> 435

```

tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgctcg 60
aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
                                         Met Asp Asn Asp Phe
                                         1                               5

gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163
Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
                        10                               15                               20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211
Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
                        25                               30                               35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
                        40                               45                               50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307
Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
                        55                               60                               65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
                        70                               75                               80                               85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403
Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
                        90                               95                               100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451
Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
                        105                               110                               115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499
Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
                        120                               125                               130

```

```

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547
Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val
    135                140                145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595
Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro
    150                155                160                165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643
Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro
                170                175                180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691
Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln
                185                190                195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739
Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys
    200                205                210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785
Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr
    215                220                225

ggcactaaga aga 798

<210> 436
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 436
Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp
  1                5                10                15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala
    20                25                30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg
    35                40                45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys
    50                55                60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile
    65                70                75                80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala
                85                90                95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu
    100                105                110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly
    115                120                125

Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly
    130                135                140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val

```

145									150									155									160
Ile	Gly	Ala	Gly	Pro	Val	Val	Thr	Lys	Asp	Ile	Pro	Asp	Asp	Ser	Ile												
				165					170						175												
Ala	Val	Gly	Asn	Pro	Ala	Arg	Val	Val	Arg	Lys	Arg	Asp	Asp	Ser	Arg												
			180					185						190													
Leu	Glu	Arg	Ser	Gln	Leu	Pro	Glu	Gly	Ala	Ser	Val	Asp	Ala	Leu	Gly												
		195					200					205															
Ile	Leu	Pro	Thr	Lys	Ser	Pro	Arg	Leu	Ser	Glu	Asn	Ile	Ala	Glu	Lys												
	210					215					220																
Tyr																											
225																											

```
<210> 437
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(868)  
<223> RXA02666
```

<400> 437																
gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga																60
tcttgacgat ctgagcttcg acgacgaaga ttagacgccc																
										atg	tcg	tct	aca	cga		115
										Met	Ser	Ser	Thr	Arg		
										1				5		
atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc																163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10					15					20		
ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt																211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			
tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa																259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
		40					45					50				
atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg																307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
		55				60					65					
ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg																355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	
		70			75					80					85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt																403
Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser	Val	Trp	Ala	Gly	Leu	
				90					95					100		
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc																451
Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp	Ala	Ile	Val	Leu	Ile	

105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg			499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val			
120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca			547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro			
135	140	145	
gta tgc gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc			595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val			
150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc			643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly			
170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac			691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp			
185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg			739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp			
200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa			787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys			
215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa			835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu			
230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg			888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp			
250	255		
tag			891

<210> 438

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met	Ser	Ser	Thr	Arg	Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly
1				5					10					15	

Arg	Gly	Thr	Arg	Leu	Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu
	20						25						30		

Arg	Glu	Arg	Thr	Leu	Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser
	35						40					45			

Glu	Ser	Val	Asp	Glu	Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr
	50				55						60				

Tyr	Ala	Arg	Asp	Leu	Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu
65					70					75					80

Gly	Val	Arg	Val	Arg	Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser
				85					90					95	
Val	Trp	Ala	Gly	Leu	Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp
			100					105					110		
Ala	Ile	Val	Leu	Ile	His	Asp	Ser	Ala	Arg	Ala	Leu	Thr	Pro	Pro	Gly
		115					120					125			
Met	Ile	Ala	Arg	Val	Val	Arg	Lys	Val	His	Glu	Gly	Ala	Thr	Ala	Val
	130					135					140				
Ile	Pro	Val	Leu	Pro	Val	Ser	Asp	Thr	Ile	Lys	Arg	Val	Ser	Pro	Asp
145					150					155					160
Gly	Gly	Val	Val	Val	Asp	Thr	Pro	Asn	Arg	Ala	Glu	Leu	Arg	Ala	Val
				165					170					175	
Gln	Thr	Pro	Gln	Gly	Phe	Leu	Leu	Ser	Glu	Leu	Val	Ala	Ala	Asn	Glu
			180					185					190		
Lys	Phe	Phe	Ala	Asp	Pro	Asn	Pro	Gly	Phe	Ile	Pro	Thr	Asp	Asp	Ala
		195					200					205			
Ser	Leu	Met	Glu	Trp	Tyr	Gly	Ala	Asp	Val	Val	Cys	Val	Gln	Gly	Asp
	210					215					220				
Pro	Met	Ala	Phe	Lys	Val	Thr	Thr	Pro	Ile	Asp	Met	Met	Leu	Ala	Gln
225					230					235					240
Arg	Ile	Thr	Asp	Glu	Ala	Glu	Pro	Thr	Ile	Phe	Glu	Val	Pro	Gly	Asp
				245					250					255	

```
<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1042)  
<223> RXA00202
```

```

<400> 439
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115
                                         Met Tyr Ala Arg Lys
                                         1                               5

ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
                        10                        15.                        20

tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp

```


25	30	35	
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val 40 45 50			259
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr 55 60 65			307
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln 70 75 80 85			355
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro 90 95 100			403
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala 105 110 115			451
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val 120 125 130			499
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala 135 140 145			547
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu 150 155 160 165			595
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe 170 175 180			643
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln 185 190 195			691
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu 200 205 210			739
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu 215 220 225			787
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp 230 235 240 245			835
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val 250 255 260			883
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu 265 270 275			931

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
 280 285 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
 295 300 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
 Val Ala Asp Phe Lys
 310

<210> 440
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 440
 Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
 1 5 10 15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140

Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 441
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(940)
 <223> RXA02440

<400> 441
 gctgttaatc acgggttggt cagctaccgg gggagcacca cgggcaacag atggggcatc 60
 aggcggagga accgtcgata cgctcgggtt ggttgctcgcg atg gtg agc cac ggc 115
 Met Val Ser His Gly
 1 5
 gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163
 Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp
 10 15 20
 gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211
 Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu
 25 30 35
 atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259
 Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val
 40 45 50
 gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307
 Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val
 55 60 65
 gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355
 Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala
 70 75 80 85
 gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403
 Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln
 90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met
200 205 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro
215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg
230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala
250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu
265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963
Gly Leu Arg
280

<210> 442

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg
1 5 10 15

Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr
20 25 30

```
<210> 443
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1459)
<223> RXN01569
```

<400> 443
aaggcctaga qcagaccatc gatttggtacc qcqaaaacga qgcctggtgg cgcctgccca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
Met Glu Tyr Gly Lys
1 5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
10 15 20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
25 30 35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
40 45 50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
55 60 65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
70 75 80 85

gga gct tgg gtg gat ctg cgc gcg ggc tcc agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
90 95 100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
105 110 115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
120 125 130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
135 140 145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
150 155 160 165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
170 175 180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
185 190 195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
200 205 210

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc	835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg	
230 235 240 245	
gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc	883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Asn Leu Ala Thr	
250 255 260	
atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat	931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr	
265 270 275	
gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc	979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser	
280 285 290	
cca ctc gcc gtg tac ggc caa tcc aaa gca gcc gcc gac atc gga gac	1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp	
295 300 305	
acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att gcc	1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly	
310 315 320 325	
gat gcc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc gcc	1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly	
330 335 340	
atc gca cca tca gta gtt gat gat caa atc gcc cgc cta tcc ttc acc	1171
Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr	
345 350 355	
gaa gac atc gca gcc gcc atc gcg cac ctt ttg gaa gtg ggt gca gca	1219
Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala	
360 365 370	
tat gcc acc tac aac ctc acc aac acc gcc gaa ccc gca agc tgg gcc	1267
Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala	
375 380 385	
gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc gcc gtg	1315
Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val	
390 395 400 405	
agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg	1363
Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu	
410 415 420	
aac tcc gtt ttg gat ctc gcc aaa atc gaa gcc acc gga ttt agc gca	1411
Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala	
425 430 435	
ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag	1459
Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys	
440 445 450	
tgaaaggcat catcctcgca ggt	1482

<210> 444

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

```

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
 1           5           10           15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
      20           25           30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
      35           40           45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
      50           55           60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
      65           70           75           80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
      85           90           95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
      100           105           110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
      115           120           125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
      130           135           140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
      145           150           155           160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
      165           170           175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
      180           185           190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
      195           200           205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
      210           215           220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
      225           230           235           240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
      245           250           255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
      260           265           270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
      275           280           285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
      290           295           300

```


Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr
 305 310 315 320
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser
 325 330 335
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly
 340 345 350
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu
 355 360 365
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu
 370 375 380
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr
 385 390 395 400
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala
 405 410 415
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala
 420 425 430
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu
 435 440 445
 Lys Glu Leu Ser Lys
 450

<210> 445
 <211> 449
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(426)
 <223> FRXA01569

<400> 445
 gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc 48
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15
 aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30
 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45
 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60
 acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

tgaaaggcat catcctcgca ggt 449

<210> 446
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum.

<400> 446
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

<210> 447
 <211> 1028
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1021)

<223> FRXA02055

<400> 447

```

aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgccca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1           5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
              10              15              20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
              25              30              35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
              40              45              50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
              55              60              65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
              70              75              80              85

gga gct tgg gtg gat ctg cgc gcg ggc tgc agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
              90              95              100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
              105              110              115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
              120              125              130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
              135              140              145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
              150              155              160              165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
              170              175              180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
              185              190              195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
              200              205              210

```

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931
 Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser
 295 300 305

taagcac 1028

<210> 448
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 448
 Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
 145 150 155 160
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
 165 170 175
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
 180 185 190
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
 195 200 205
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
 210 215 220
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
 225 230 235 240
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
 245 250 255
 Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr
 260 265 270
 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys
 275 280 285
 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro
 290 295 300
 Ala Thr Ser
 305

<210> 449
 <211> 1056
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1033)
 <223> RXA00825

<400> 449
 cccgttcacg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60
 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
 Met Arg Thr Val Val
 1 5
 acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
 10 15 20
 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
 Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
 25 30 35
 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
 Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val

40	45	50	
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His 55 60 65			307
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 80 85			355
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr 90 95 100			403
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 110 115			451
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 125 130			499
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 140 145			547
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 160 165			595
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 175 180			643
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 190 195			691
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg 200 205 210			739
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 215 220 225			787
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245			835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260			883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275			931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290			979

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
 1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240

Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255

Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270

Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285

Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300

Val Glu Tyr Phe Arg Thr His
 305 310

<210> 451
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXA02054

<400> 451
 cctaataaac agccggagca ccctggctgt ttgcagaata ggcgcacgca caacagctac 60

taactctgcc agctcgcccg gacgaactaa ggtagacggc atg act tct ttg ctt 115
 Met Thr Ser Leu Leu
 1 5

gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc 163
 Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr
 10 15 20

gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc 211
 Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu
 25 30 35

acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa 259
 Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys
 40 45 50

gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc 307
 Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser
 55 60 65

ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac 355
 Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His
 70 75 80 85

aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc 403
 Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu
 90 95 100

atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc 451
 Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg
 105 110 115

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat 499
 Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp
 120 125 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca 547
 Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro
 135 140 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc 595
 Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile
 150 155 160 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac 643
 Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr
 170 175 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat 691
 Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn
 185 190 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc 739
 Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val
 200 205 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc 787
 Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile
 215 220 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn
 230 235 240 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met
 250 255 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His
 265 270 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly
 280 285 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu
 295 300 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro
 310 315 320 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln
 330 335

taatggaata cggtaaacaa etc 1140

<210> 452

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

```

Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn
  1           5           10           15

Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
      20           25           30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
      35           40           45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
      50           55           60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
      65           70           75           80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
      85           90           95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
      100          105          110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
      115          120          125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
      130          135          140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
      145          150          155          160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
      165          170          175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
      180          185          190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
      195          200          205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
      210          215          220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
      225          230          235          240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
      245          250          255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
      260          265          270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
      275          280          285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
      290          295          300

```

Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu
 305 310 315 320

Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys
 325 330 335

Gln Gly Gln

<210> 453

<211> 909

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXN00427

<400> 453

gcggtcattg tgaccacaaa tcgtgtggaa ttgctgcggc attccctcga ggttgttgcc 60

aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta 115
 Met Gly Arg Ile Leu
 1 5

gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163
 Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr
 10 15 20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt 211
 Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly
 25 30 35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac 259
 Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp
 40 45 50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac 307
 Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp
 55 60 65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat 355
 Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn
 70 75 80 85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag 403
 Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu
 90 95 100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat 451
 Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp
 105 110 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc 499
 Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser
 120 125 130

gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att 547
 Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile

135	140	145	
cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg			595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu			
150	155	160	165
ccg ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct			643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser			
	170	175	180
gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg			691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro			
	185	190	195
gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg			739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu			
	200	205	210
atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc			787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg			
	215	220	225
ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg			835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg			
230	235	240	245
gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg			883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg			
	250	255	260
ccc tagatcagtt ttagtagttc ctc			909
Pro			

<210> 454

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly
1 5 10 15

Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly
20 25 30

Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
35 40 45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
50 55 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu
85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn
 115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp
 130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu
 145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu
 165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met
 180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg
 195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro
 210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp
 225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp
 245 250 255

Glu Lys Phe Asn Arg Pro
 260

<210> 455
 <211> 555
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(532)
 <223> FRXA00427

<400> 455
 tgctgatgat ccggagcggg tggcatttcc gctgcgtcgg ggcttggagt ggcgtcggat 60

gcgcagtgag ttgattgata cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115
 Leu Leu Pro Gly Ile
 1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163
 Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg
 10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211
 Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu
 25 30 35

tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259
 Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu
 40 45 50

acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307
 Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile
 55 60 65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355
 Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg
 70 75 80 85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403
 Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met
 90 95 100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451
 Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu
 105 110 115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499
 Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His
 120 125 130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552
 Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
 135 140

ctc 555

<210> 456

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala
 1 5 10 15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg
 20 25 30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro
 35 40 45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp
 50 55 60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp
 65 70 75 80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met
 85 90 95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe
 100 105 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu
 115 120 125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
 130 135 140

```
<210> 457
<211> 507
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(484)  
<223> RXA00327
```

<400> 457																			
aacgatttttc	gccgctcgcaa	ccgtgatcac	cggtcgcttt	ccggcatcgt	gtcgtcgcg	60													
ctaggggggcc						aggcgcgga	tgattgggtt	tgtcacgccg	atg	att	cag	gcg	gcg	115					
									Met	Ile	Gln	Ala	Ala	5					
									1										
ttg	tgg	atc	gtg	ctc	ttt	tta	ttc	gct	gat	cgc	ctg	tcc	aat	ccg	ctg	163			
Leu	Trp	Ile	Val	Leu	Phe	Leu	Phe	Ala	Asp	Arg	Leu	Ser	Asn	Pro	Leu				
						10						15						20	
gtt	ttt	gtc	agc	gcc	atc	atg	ttc	gcg	att	tcc	ttt	agc	tcc	ccc	gtg	211			
Val	Phe	Val	Ser	Ala	Ile	Met	Phe	Ala	Ile	Ser	Phe	Ser	Ser	Pro	Val				
						25						30						35	
gcg	aac	ttc	ggg	ttc	gat	acg	atc	tgc	gaa	aaa	ctc	gac	cgc	cgc	gtc	259			
Ala	Asn	Phe	Gly	Phe	Asp	Thr	Ile	Cys	Glu	Lys	Leu	Asp	Arg	Arg	Val				
						40						45						50	
atg	gtc	gcc	ggc	acc	ggc	atg	gcc	aac	atg	agc	gcc	tac	att	tgc	gcg	307			
Met	Val	Ala	Gly	Thr	Gly	Met	Ala	Asn	Met	Ser	Ala	Tyr	Ile	Cys	Ala				
						55						60						65	
atg	ctg	gcc	aca	caa	atc	atc	gga	ttt	tta	ctc	gac	tgg	aac	gcc	gac	355			
Met	Leu	Ala	Thr	Gln	Ile	Ile	Gly	Phe	Leu	Leu	Asp	Trp	Asn	Ala	Asp				
						70						75						80	85
ggc	cac	gcc	tac	acc	tgg	tcg	aat	ttc	cag	gtg	gcg	tgg	ctt	ggg	ctg	403			
Gly	His	Ala	Tyr	Thr	Trp	Ser	Asn	Phe	Gln	Val	Ala	Trp	Leu	Gly	Leu				
						90						95						100	
ggc	gcg	gtg	tgg	ctg	gca	ggc	atg	atc	ggg	ctt	gca	gtc	tgc	ctc	ctg	451			
Gly	Ala	Val	Trp	Leu	Ala	Gly	Met	Ile	Gly	Leu	Ala	Val	Cys	Leu	Leu				
						105						110						115	
ctg	cag	cgt	cga	aaa	aat	att	gct	ttt	cga	cgc	taaaaccgga	ccgtaaccgc	504						
Leu	Gln	Arg	Arg	Lys	Asn	Ile	Ala	Phe	Arg	Arg									
						120						125							
taq																507			

```
<210> 458
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg
 1 5 10 15
 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
 20 25 30
 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
 35 40 45
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
 50 55 60
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
 65 70 75 80
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
 85 90 95
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
 100 105 110
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
 115 120 125

<210> 459
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00328

<400> 459
 gtcacgggat ttgttgtagc ccgactcaag ggtggaccgg gccgcagatt actcgcccag 60
 attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115
 Val Gly Val Glu Arg
 1 5
 ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163
 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys
 10 15 20
 gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211
 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly
 25 30 35
 gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cgg ttg gcc gtg 259
 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val
 40 45 50
 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307
 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met
 55 60 65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355
 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly
 70 75 80 85
 gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct 403
 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser
 90 95 100
 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451
 Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser
 105 110 115
 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499
 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met
 120 125 130
 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547
 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val
 135 140 145
 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592
 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro
 150 155 160
 taggggtggac aattcctttc gca 615

<210> 460

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 460

Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp
 1 5 10 15
 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser
 20 25 30
 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala
 35 40 45
 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu
 50 55 60
 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys
 65 70 75 80
 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu
 85 90 95
 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile
 100 105 110
 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro
 115 120 125
 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly
 130 135 140
 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr

145

150

155

160

Tyr Ser Thr Pro

<210> 461

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXA00329

<400> 461

tgtgaagaac aatgatcaac ggccttcgcc aagaccgcat cccagagaga aagtaactac 60

ccgcgccttc atagtttggg cagcagcctg tcttgtgtat atg gca gcc att acc 115
 Met Ala Ala Ile Thr
 1 5

agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt 163
 Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe
 10 15 20

cag gta gac gcc aca cgc att gca gta ttc act tct gtt cag gtt ggt 211
 Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr Ser Val Gln Val Gly
 25 30 35

gtg tac gcg ttt gct cag att ccg atg ggc att ttg atc gat aag ttt 259
 Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile Leu Ile Asp Lys Phe
 40 45 50

ggc cct cgg aag ctc ctt gcc att ggt gct ttg gtg atg ggt atc ggc 307
 Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu Val Met Gly Ile Gly
 55 60 65

cag ctc att ttg ggc ttt acg gat agc tat tcc atc gcg att att gcc 355
 Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser Ile Ala Ile Ile Ala
 70 75 80 85

cgc gtg ttt atc ggc gcc ggc gat gca tcg atc ttc ctt tcg gtt atg 403
 Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile Phe Leu Ser Val Met
 90 95 100

cgc atc ctg ccg ttt tgg ttc cca ctg aag cac acc cct att ttc acg 451
 Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His Thr Pro Ile Phe Thr
 105 110 115

cag tta act acc tgc ctt ggc cag ttg ggc cag ttc ttt tct gcg gtg 499
 Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln Phe Phe Ser Ala Val
 120 125 130

cct ttc atg gcg ttg ttg ggt gcg cag ggt tgg cct gtg gcg ttt gtc 547
 Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val
 135 140 145

agc ctt ggt tcc gtg gtg gca ctc att gcg atc gca gcg ctg gtg gcc 595
 Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala

150	155	160	165	
gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag	643			
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln				
170	175	180		
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc	691			
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg				
185	190	195		
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg	739			
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val				
200	205	210		
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg	787			
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu				
215	220	225		
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac	835			
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn				
230	235	240	245	
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca	883			
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala				
250	255	260		
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt	931			
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val				
265	270	275		
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt	979			
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly				
280	285	290		
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg	1027			
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala				
295	300	305		
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag	1075			
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys				
310	315	320	325	
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca	1123			
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser				
330	335	340		
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg	1171			
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala				
345	350	355		
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg	1219			
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala				
360	365	370		
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga	1267			
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg				
375	380	385		
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc	1315			
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr				
390	395	400	405	

aag gac ttt taaagatcgg gtaaacctg tgg
Lys Asp Phe

1347

<210> 462

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu
1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr
20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile
35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu
50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser
65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile
85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His
100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln
115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp
130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile
145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro
165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu
180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His
195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val
210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu
225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile
245 250 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

260	265	270
Ala Leu Ser Phe Val Gln Ser	Ala Val Trp Leu Val Phe Leu Ala Ser	
275	280	285
Asp Ala Pro Arg Gly Leu Met	Ala Ile Ile Leu Val Asn Ile Val Met	
290	295	300
Gly Leu Thr Thr Ala Ala Ser	Gly Tyr Gly Phe Asp Thr Ile Arg Glu	
305	310	315
Arg Leu Asp Arg Lys Ile Leu	Ala Ala Gly Thr Gly Leu Ala Asn Met	
325	330	335
Gly Gly Phe Leu Ser Ser Met	Val Ala Ala Gln Val Met Gly Phe Leu	
340	345	350
Leu Asp His Ser Ala His Gly	Ser Thr Tyr Thr Trp Val Asp Phe Arg	
355	360	365
Phe Gly Phe Leu Ala Ile Leu	Val Thr Trp Ala Val Gly Val Thr Gly	
370	375	380
Phe Val Val Ala Arg Leu Lys	Gly Gly Pro Gly Arg Arg Leu Leu Ala	
385	390	395
Gln Ile Arg Ser Thr Lys Asp	Phe	
405		

<210> 463

<211> 2265

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2242)

<223> RXN01554

<400> 463

tggtctaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaa 60

tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115
 Leu Lys Lys His Val
 1 5

acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163
 Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
 10 15 20

ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211
 Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
 25 30 35

gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259
 Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser
 40 45 50

gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307
 Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly

55	60	65	
agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly 70 75 80 85			355
aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala 90 95 100			403
atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln 105 110 115			451
gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg 120 125 130			499
atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr 135 140 145			547
gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp 150 155 160 165			595
atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu 170 175 180			643
tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser 185 190 195			691
cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val 200 205 210			739
aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 220 225			787
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val 230 235 240 245			835
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 250 255 260			883
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 265 270 275			931
cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290			979
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu 295 300 305			1027

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga	1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly	
310 315 320 325	
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt	1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu	
330 335 340	
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa	1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu	
345 350 355	
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc	1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser	
360 365 370	
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag	1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu	
375 380 385	
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg	1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val	
390 395 400 405	
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa	1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Ile Ala Thr Pro Glu	
410 415 420	
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
505 510 515	
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
520 525 530	
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc	1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc 1795
 Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
 550 555 560 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag 1843
 Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
 570 575 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt 1891
 Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
 585 590 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca 1939
 Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
 600 605 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac 1987
 Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
 615 620 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct 2035
 His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
 630 635 640 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat 2083
 Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
 650 655 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
 665 670 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
 680 685 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
 695 700 705

atg aga cag ttc aag taatccttgt gggcgctttg tct 2265
 Met Arg Gln Phe Lys
 710

<210> 464

<211> 714

<212> PRT

<213> Corynebacterium glutamicum

<400> 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
 1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg

50					55					60					
Gln	Pro	Asp	Tyr	Gly	Ser	Asp	Lys	Val	Leu	Tyr	Thr	Glu	Asp	Ala	Leu
65					70					75					80
Ser	Ile	Glu	Asp	Gly	Lys	Leu	Thr	Ile	Thr	Thr	Gln	Arg	His	Cys	Val
				85					90					95	
Asp	Glu	Asp	Phe	Ala	Ile	Ser	Asp	Pro	Val	Asn	Arg	Gly	Lys	Leu	Asn
			100					105					110		
Asp	Ser	Thr	Ala	Gln	Val	Glu	Pro	Cys	Ala	Pro	Gly	Gln	Phe	Glu	Lys
			115				120					125			
Phe	Thr	Ser	Ala	Arg	Ile	Val	Thr	Pro	Lys	Ile	Ala	Arg	Gly	Glu	Phe
			130				135					140			
Asp	Leu	Ser	Val	Thr	Ala	Thr	Leu	Asn	Thr	Gly	Gly	Val	Glu	Gly	Val
145					150					155					160
Arg	Ser	Ala	Ile	Trp	Met	Gln	Asn	Gly	Glu	Gln	Ala	Cys	Ser	Ser	Ala
			165						170					175	
Thr	Asn	Asn	Gly	Leu	Tyr	Gly	Glu	Leu	Asp	Leu	Val	Glu	His	Phe	Ser
			180					185					190		
Tyr	Asp	Leu	Arg	Ser	Pro	Trp	Ser	Pro	Ser	Asn	Thr	His	Leu	Gly	Cys
		195					200					205			
Asp	Pro	Glu	Ser	Val	Asn	Gly	Thr	Asn	Arg	Ala	Pro	Arg	Glu	Leu	Lys
		210				215					220				
Leu	Asp	Glu	Ser	Leu	Asp	Gly	Val	Glu	His	Thr	Trp	Thr	Val	Ser	Thr
225					230					235					240
Thr	Arg	Asp	Gly	Val	Glu	Tyr	Phe	Ile	Asp	Asp	Glu	Ala	Ile	Asn	Arg
			245						250					255	
Gln	Ser	Trp	Arg	Asn	Asp	Val	Thr	Leu	Gly	His	Ala	Glu	Ile	Asp	Asp
			260					265					270		
Phe	Gly	Ile	Ser	Ala	Gln	Thr	Phe	Asp	Glu	Ile	Val	Asp	Arg	Glu	Trp
		275					280					285			
Thr	Leu	Thr	Leu	Asn	Gln	Lys	Val	Glu	Ser	Ala	Asp	Trp	Ala	Lys	Pro
		290				295					300				
Arg	Ser	Ser	Glu	Glu	Asp	Phe	Pro	Val	Arg	Ser	Met	Val	Ile	Asp	Arg
305					310					315					320
Ile	Glu	Val	Thr	Gly	Ser	Pro	Ala	Val	Ser	Glu	Asp	Thr	Pro	Met	Pro
				325					330					335	
Asp	Thr	Thr	Gln	Leu	Leu	Thr	Gln	Asp	Thr	Leu	Glu	Tyr	Leu	Gly	Arg
			340				345					350			
Met	Pro	Val	Leu	Glu	Arg	Tyr	Glu	Pro	Ala	Ser	Ala	Asp	Phe	Ala	Asp
		355					360					365			
Gly	Arg	Arg	Pro	Ser	Trp	Asn	Tyr	Phe	Asn	Leu	Lys	Glu	Ser	Trp	Gln
				370		375					380				

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
 385 390 395 400
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
 405 410 415
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
 420 425 430
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
 435 440 445
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
 450 455 460
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
 465 470 475 480
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
 485 490 495
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
 500 505 510
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
 515 520 525
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
 530 535 540
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
 545 550 555 560
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
 565 570 575
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
 580 585 590
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
 595 600 605
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
 610 615 620
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
 625 630 635 640
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
 645 650 655
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
 660 665 670
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
 675 680 685
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
 690 695 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705 710

<210> 465
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXN03015

<400> 465
ccgggtttgc ctgaggtttt ggagcgcaat ctggaaaatg gtcgcctgaa cttcactact 60

gattatgcgg aggctgcggc ttctgcgcag gtgcatttct ttg ggc gtg ggt act . 115
Leu Gly Val Gly Thr
1 5

cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln
10 15 20

gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
25 30 35

ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
40 45 50

gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
55 60 65

ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
70 75 80 85

gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389
Asp Arg Ile Val Val Gly Val Arg Glu
90

<210> 466
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 466
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu
1 5 10 15

Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly
20 25 30

Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu
35 40 45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val
 50 55 60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys
 65 70 75 80

Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu
 85 90

<210> 467
 <211> 801
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(778)
 <223> RXN03056

<400> 467
 ttactatcac tggttttgca gatgagatcg cacatgatct cgacgaacag atttccttac 60

ttaataaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga 115
 Leu Asp Ala Ala Gly
 1 5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163
 Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr
 10 15 20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211
 Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val
 25 30 35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259
 Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile
 40 45 50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307
 Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg
 55 60 65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355
 Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu
 70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403
 His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys
 90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451
 Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp
 105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499
 Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp
 120 125 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc 547
 Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr

135	140	145	
att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa			595
Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln			
150	155	160	165
ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt			643
Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly			
	170	175	180
tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa			691
Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu			
	185	190	195
ttc ggc gga ctc tgc gga cct gac ctg tgg acc agc gca tgc gac gct			739
Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala			
	200	205	210
ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac			788
Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn			
	215	220	225
tgataatgac aaa			801
<210> 468			
<211> 226			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 468			
Leu Asp Ala Ala Gly Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly			
1	5	10	15
Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg			
	20	25	30
His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met			
	35	40	45
Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys			
	50	55	60
Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly			
	65	70	75
Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser			
	85	90	95
Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr			
	100	105	110
Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro			
	115	120	125
Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His			
	130	135	140
Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile			
	145	150	155
			160

<400> 469															
gaagatgaag cagaaaagat catttggtgcg ccagagggttt ctgcattggg caacaaagca 60															
cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115															
Val Leu Pro Leu Asp 5															
1															
cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163															
Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys 20															
10 15															
atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211															
Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu 35															
25 30															
cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259															
Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile 50															
40 45															
gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307															
Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly 65															
55 60															
gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355															
Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg 85															
70 75 80															
gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403															
Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe 100															
90 95															
acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg 451															
Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Ala Val 105 110 115															

gtg ggc act ttt gag atc aag cca gag ttc ctt ctc aag gct ttg act 499
 Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu Leu Lys Ala Leu Thr
 120 125 130

ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct 547
 Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala
 135 140 145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc 595
 Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe
 150 155 160 165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag 643
 Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys
 170 175 180

tac ggt cac gga ctt aat ttc tagattgtag gtagtctcgt ggg 687
 Tyr Gly His Gly Leu Asn Phe
 185

<210> 470

<211> 188

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 470

Val Leu Pro Leu Asp Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val
 1 5 10 15

Thr Gly Arg Thr Lys Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala
 20 25 30

Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu
 35 40 45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu
 50 55 60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly
 65 70 75 80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile
 85 90 95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro
 100 105 110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu
 115 120 125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro
 130 135 140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp
 145 150 155 160

Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala
 165 170 175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe

Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys
 170 175 180
 atc acc acg cta tgc gga gat cgc ctg ttc tac ctc ggt gga ctt ccc 691
 Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro
 185 190 195
 acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc 739
 Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr
 200 205 210
 tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc 787
 Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe
 215 220 225
 tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg 835
 Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu
 230 235 240 245
 agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc 883
 Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly
 250 255 260
 tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac 931
 Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn
 265 270 275
 gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc 979
 Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile
 280 285 290
 gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg
 295 300 305
 ctt cag ttg agg tgaaagcatg atcaccgcaa ccg 1062
 Leu Gln Leu Arg
 310

<210> 472

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly
 1 5 10 15
 Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp
 20 25 30
 Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val
 35 40 45
 Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr
 50 55 60
 Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser
 65 70 75 80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala
 85 90 95

Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu
 100 105 110

Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn
 115 120 125

His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr
 130 135 140

Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser
 145 150 155 160

Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile
 165 170 175

Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr
 180 185 190

Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln
 195 200 205

Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp
 210 215 220

Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala
 225 230 235 240

Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg
 245 250 255

Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys
 260 265 270

Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu
 275 280 285

Ser Glu Gln Asp Ile Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly
 290 295 300

Ala Gly Ser Tyr Arg Leu Gln Leu Arg
 305 310

<210> 473

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXN02125

<400> 473

gacctaataat tcatacacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60

gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
 Met Val Ala Thr Ser

1															5	
cag	ttt	atc	gat	gac	agc	gag	gct	gcc	cag	gcg	gta	cgc	gca	gct	att	163
Gln	Phe	Ile	Asp	Asp	Ser	Glu	Ala	Ala	Gln	Ala	Val	Arg	Ala	Ala	Ile	
				10					15					20		
gtt	gca	gga	tac	cga	aac	att	gat	act	gcc	cta	gcg	tat	gga	aac	gag	211
Val	Ala	Gly	Tyr	Arg	Asn	Ile	Asp	Thr	Ala	Leu	Ala	Tyr	Gly	Asn	Glu	
			25					30					35			
cgc	ggc	gtt	ggc	gaa	ggc	att	cgc	acc	gct	gga	gtg	ccc	cgc	gag	gag	259
Arg	Gly	Val	Gly	Glu	Gly	Ile	Arg	Thr	Ala	Gly	Val	Pro	Arg	Glu	Glu	
		40					45					50				
ctc	ttt	att	tcc	acc	aag	cta	gct	gca	gaa	atc	aaa	gat	tac	gat	gga	307
Leu	Phe	Ile	Ser	Thr	Lys	Leu	Ala	Ala	Glu	Ile	Lys	Asp	Tyr	Asp	Gly	
	55					60					65					
gca	gtc	gcc	gcg	att	gat	gag	tct	ttg	gcg	aaa	att	ggc	ttg	gat	tat	355
Ala	Val	Ala	Ala	Ile	Asp	Glu	Ser	Leu	Ala	Lys	Ile	Gly	Leu	Asp	Tyr	
	70				75					80				85		
gtc	gat	ctg	atg	ctc	att	cac	tcc	cca	caa	cca	tgg	agt	gat	ttc	cgt	403
Val	Asp	Leu	Met	Leu	Ile	His	Ser	Pro	Gln	Pro	Trp	Ser	Asp	Phe	Arg	
				90					95					100		
ggt	ggg	gac	tat	tca	gag	gga	aac	cgt	gaa	gcg	tgg	cgc	gcg	ctg	gaa	451
Gly	Gly	Asp	Tyr	Ser	Glu	Gly	Asn	Arg	Glu	Ala	Trp	Arg	Ala	Leu	Glu	
		105						110					115			
gat	gcc	tac	aaa	gcc	gga	aag	att	cga	tcc	att	ggt	gtc	tcg	aac	ttc	499
Asp	Ala	Tyr	Lys	Ala	Gly	Lys	Ile	Arg	Ser	Ile	Gly	Val	Ser	Asn	Phe	
		120					125					130				
ctg	gag	gcc	gat	ctg	gag	aat	atc	tta	gac	tcc	gcg	acg	gtt	gct	cct	547
Leu	Glu	Ala	Asp	Leu	Glu	Asn	Ile	Leu	Asp	Ser	Ala	Thr	Val	Ala	Pro	
	135					140					145					
cac	gtt	aat	cag	ctt	ctt	gtg	cat	gtt	gga	aac	acc	cca	agc	gag	tta	595
His	Val	Asn	Gln	Leu	Leu	Val	His	Val	Gly	Asn	Thr	Pro	Ser	Glu	Leu	
	150				155					160					165	
atc	agt	ttc	tgc	gat	tcc	aag	ggc	att	ctg	gtc	gaa	gca	tat	tca	ccc	643
Ile	Ser	Phe	Cys	Asp	Ser	Lys	Gly	Ile	Leu	Val	Glu	Ala	Tyr	Ser	Pro	
				170					175					180		
atc	gcc	cac	gga	gag	atg	ctg	aag	aac	cag	cag	gtc	aag	gcg	att	gct	691
Ile	Ala	His	Gly	Glu	Met	Leu	Lys	Asn	Gln	Gln	Val	Lys	Ala	Ile	Ala	
			185					190					195			
gac	aag	tac	aac	gtg	agc	att	ccg	cag	cta	tgc	att	cgg	tac	aca	att	739
Asp	Lys	Tyr	Asn	Val	Ser	Ile	Pro	Gln	Leu	Cys	Ile	Arg	Tyr	Thr	Ile	
		200					205					210				
caa	ctg	gga	acg	gtg	tct	ttg	cca	aag	act	gcc	aac	cca	gat	cat	atg	787
Gln	Leu	Gly	Thr	Val	Ser	Leu	Pro	Lys	Thr	Ala	Asn	Pro	Asp	His	Met	
	215					220					225					
agc	tcc	aat	gcg	cag	atc	gac	ttt	gaa	att	tcc	gag	gaa	gac	atg	gcg	835
Ser	Ser	Asn	Ala	Gln	Ile	Asp	Phe	Glu	Ile	Ser	Glu	Glu	Asp	Met	Ala	
	230				235					240				245		

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt 883
 Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
 250 255 260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924
 Pro Val Tyr Ser Gly Lys
 265

<210> 474

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
 1 5 10 15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
 20 25 30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
 35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
 50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
 85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
 100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
 115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
 130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
 145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
 165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
 180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
 195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
 210 215 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
 225 230 235 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
 245 250 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
 260 265

<210> 475

<211> 3561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3538)

<223> RXN00200

<400> 475

aacccggagt catttgatca gatgtggcag accaagcaag tgggaccttt cgtggtggta 60

acgcacaatg agtaattcct caccaaacga cccaagccct atg cgc caa gtc ggt 115
 Met Arg Gln Val Gly
 1 5

ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163
 Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val
 10 15 20

gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc 211
 Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala
 25 30 35

ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg 259
 Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu
 40 45 50

ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct 307
 Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser
 55 60 65

tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg 355
 Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro
 70 75 80 85

ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc 403
 Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser
 90 95 100

gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg 451
 Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu
 105 110 115

cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc 499
 Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr
 120 125 130

atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat 547
 Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp
 135 140 145

ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag 595

Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu 150 155 160 165	
att tcc tcc acc gag gaa acc acc agc gcg gaa atc acc ggc acg gca Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala 170 175 180	643
ttc agc ggc gag acc gaa ggc gat gag cgg cct cag gtc acc ggc gtt Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val 185 190 195	691
tac acc gag ctt gtc gac gac ccc tcc acc gca tcg gcc ctg gcc tca Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser 200 205 210	739
gcg ggc tta aac gtt gat att gag atc aac tcc cgc ttc act tca tcc Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser 215 220 225	787
ccc agc ctt cta aag tac gca gcc atc ttc att ggc ctt gcg tct gtg Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val 230 235 240 245	835
ttg gtc tcc ctg tgg aca ctg cac cgc atg gat att ttg gat ggt cga Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg 250 255 260	883
aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr Lys Leu Lys Pro Leu 265 270 275	931
gat ggt gtt gtc gta gcg att ttg gtg ttc tgg cac ttc ctt ggc gcc Asp Gly Val Val Val Ala Ile Leu Val Phe Trp His Phe Leu Gly Ala 280 285 290	979
aac acc tct gac gac ggc ttc atc atg acc atg gcc cgc gtg tcc cag Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met Ala Arg Val Ser Gln 295 300 305	1027
aac gcg gat tat atg gcc aac tac tac cgc tgg ttc ggt gtc cca gaa Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp Phe Gly Val Pro Glu 310 315 320 325	1075
tca cca ttc ggc gca cca tat tac gac ttg ctg gct ctg atg gcc tac Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu Ala Leu Met Ala Tyr 330 335 340	1123
atc tca acc tca tca atc tgg ctt cgt cta ccc gca ttg ctc gct gga Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro Ala Leu Leu Ala Gly 345 350 355	1171
ctg atc atg tgg ttc gtg atc acc aga gag gtc atg cca cgg ttt ggc Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val Met Pro Arg Phe Gly 360 365 370	1219
tca ttg gtt aac ggt cgc cgc gtt gcg cac tgg tct gca gcc atg gtg Ser Leu Val Asn Gly Arg Arg Val Ala His Trp Ser Ala Ala Met Val 375 380 385	1267
ttc ctg gcg ttc tgg ctt cca tac aac aac ggc act cgc cca gag cca Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly Thr Arg Pro Glu Pro	1315

390	395	400	405	
atc atc gcg atg gga gct cta ctt gcg tgg gtt tcc ttc gag cgc gct Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val Ser Phe Glu Arg Ala 410 415 420				1363
atc gct acc tcc agg ttg ttg ccc gct gcc att ggt gtc att atc gcc Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile Gly Val Ile Ile Ala 425 430 435				1411
acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu Met Ala Val Ala Ala 440 445 450				1459
ttg ctg gtc agt ttg tcc gcg ttg att cgc att ctt tat agg cgc ttg Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile Leu Tyr Arg Arg Leu 455 460 465				1507
ccg ctt att ggg gcg tcg agg ggg gcg tcg aaa agc aaa gtc ttt ggc Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys Ser Lys Val Phe Gly 470 475 480 485				1555
gct tcg atg gct atg ctt gcc cca ttc ctt gcg tct ggc acc gcg att Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala Ser Gly Thr Ala Ile 490 495 500				1603
ctc atc gcc gtt ttt ggc gat cag act ctg tca acc gtc atg gaa tcc Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser Thr Val Met Glu Ser 505 510 515				1651
atc agc gtg cgc tcc gcg aag ggc ccg gca ctg acc tgg tac cac gaa Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu Thr Trp Tyr His Glu 520 525 530				1699
tat gtg cgc tac caa acc gtc atg gaa caa acc gtt gat ggt tcc ttc Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr Val Asp Gly Ser Phe 535 540 545				1747
acc cgc cgt ttt gct gtg ctg atg ctc atg gcg tgt ctg gct att gtg Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala Cys Leu Ala Ile Val 550 555 560 565				1795
gtc atc gcg atc ctg cgt tac ggc cgc att cca ggc gct gcg aag gga Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro Gly Ala Ala Lys Gly 570 575 580				1843
cca tca ctg cgt ttg atg atg gtc att ttc ggc acc atg ttc ttc atg Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly Thr Met Phe Phe Met 585 590 595				1891
atg ttc acc cca acc aag tgg act cac cac ttc ggt gtc tac gca gga Met Phe Thr Pro Thr Lys Trp Thr His His Phe Gly Val Tyr Ala Gly 600 605 610				1939
ctt gcc ggc gca ttg gcc gga ctt gct gcc gtg ggg ctg tcc tat gtt Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val Gly Leu Ser Tyr Val 615 620 625				1987
gcg gtg aaa tca cca cgc atg cgc acc att tcc atc ggt gcg ttc ctc Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser Ile Gly Ala Phe Leu 630 635 640 645				2035

ttc ctg ctg gcg ctg gct ctc gca ggc gtg aac gga ttc tgg tac acc	2083
Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr	
650 655 660	
tcc agc tac gcc gtg cca tgg tgg gat aaa acc atc cag atc aag ggc	2131
Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly	
665 670 675	
atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc	2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile	
680 685 690	
atc ggt gtt att caa tcc ttt gtc cac gat gtg aaa acc gcg caa gcc	2227
Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala	
695 700 705	
gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag	2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys	
710 715 720 725	
cgc gag cgt gcc tcc agg ttc acc ggc ctt gcg gcc tcc cct atc gca	2323
Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala	
730 735 740	
gga gtg tcc gcc ctc gtt gtg ctg att acc tgc gca tcc atg ggc aaa	2371
Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys	
745 750 755	
ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc	2419
Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu	
760 765 770	
cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg	2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu	
775 780 785	
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt	2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu	
790 795 800 805	
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc	2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly	
810 815 820	
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt	2611
Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly	
825 830 835	
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa	2659
Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu	
840 845 850	
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa	2707
Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu	
855 860 865	
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc	2755
Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr	
870 875 880 885	

caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca	2803
Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala	
890 895 900	
aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca	2851
Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala	
905 910 915	
ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc	2899
Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile	
920 925 930	
aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc	2947
Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg	
935 940 945	
ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac	2995
Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr	
950 955 960 965	
gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac	3043
Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp	
970 975 980	
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc	3091
Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val	
985 990 995	
aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct	3139
Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro	
1000 1005 1010	
aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc	3187
Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu	
1015 1020 1025	
ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac	3235
Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp	
1030 1035 1040 1045	
cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac	3283
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp	
1050 1055 1060	
cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc	3331
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly	
1065 1070 1075	
gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg	3379
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro	
1080 1085 1090	
tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc	3427
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg	
1095 1100 1105	
tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac	3475
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp	
1110 1115 1120 1125	
atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat	3523

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
 1130 1135 1140

atg aag gta gat gaa taagaccttc agtactggaa gtt 3561
 Met Lys Val Asp Glu
 1145

<210> 476

<211> 1146

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Met Arg Gln Val Gly Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn
 1 5 10 15

Val Ser Asp Val Val Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu
 20 25 30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser
 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val
 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser
 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala
 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu
 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
 115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly
 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp
 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
 165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro
 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala
 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser
 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile
 225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp
 245 250 255

Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr
 260 265 270
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp
 275 280 285
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met
 290 295 300
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp
 305 310 315 320
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu
 325 330 335
 Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro
 340 345 350
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val
 355 360 365
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp
 370 375 380
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly
 385 390 395 400
 Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val
 405 410 415
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile
 420 425 430
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu
 435 440 445
 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile
 450 455 460
 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys
 465 470 475 480
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala
 485 490 495
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser
 500 505 510
 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu
 515 520 525
 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr
 530 535 540
 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala
 545 550 555 560
 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro
 565 570 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly
 580 585 590
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe
 595 600 605
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val
 610 615 620
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser
 625 630 635 640
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn
 645 650 655
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
 660 665 670
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala
 675 680 685
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val
 690 695 700
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala
 705 710 715 720
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala
 725 730 735
 Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys
 740 745 750
 Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val
 755 760 765
 Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala
 770 775 780
 Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro
 785 790 795 800
 Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly
 805 810 815
 Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp
 820 825 830
 Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr
 835 840 845
 Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly
 850 855 860
 Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe
 865 870 875 880
 Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly
 885 890 895
 Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu

```
<210> 477
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1486)
<223> RXN01175
```

<400> 477
tcgcgtctct tagtcgatct gctcccatcc cataagtttg gagaaaaactt aactgtttatt 60

ccattcctta aaacaccgat atcgtgctat gaataggggt	gtg agt tgg aca gtt	115
	Val Ser Trp Thr Val	
	1 5	
gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc	163	
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly		
	10 15 20	
atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa	211	
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln		
	25 30 35	
cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag	259	
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu		
	40 45 50	
tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag	307	
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln		
	55 60 65	
aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt	355	
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly		
	70 75 80 85	
gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc	403	
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala		
	90 95 100	
aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca	451	
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala		
	105 110 115	
tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag	499	
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys		
	120 125 130	
cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc	547	
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly		
	135 140 145	
gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat	595	
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp		
	150 155 160 165	
cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac	643	
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn		
	170 175 180	
ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc	691	
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu		
	185 190 195	
agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc	739	
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg		
	200 205 210	
tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa	787	
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu		
	215 220 225	
gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc	835	

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys 230 235 240 245	
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu 250 255 260	883
gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His 265 270 275	931
cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val 280 285 290	979
aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt cct Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro 295 300 305	1027
ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro 310 315 320 325	1075
aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp 330 335 340	1123
aag gtt cgc tcc gta ctt cct ggt gtt atc cag gct gtt gag gca tcc Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser 345 350 355	1171
gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe 360 365 370	1219
acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp 375 380 385	1267
gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro 390 395 400 405	1315
ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu 410 415 420	1363
ggt ggc gct gaa gac atc acc gat gtt gat ctg cca ggc cgc tac gag Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu 425 430 435	1411
tcc gca tgc gat cct cgc ctg aac act cag cag tct ttg gag ttg gct Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala 440 445 450	1459
ttc ctc gtt gca gaa atg ctg cgt aac taagctttta gaccaactct Phe Leu Val Ala Glu Met Leu Arg Asn 455 460	1506
aaa	1509

<210> 478
 <211> 462
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478

```

Val Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro
 1           5           10           15

Pro Leu Pro Glu Gly Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg
      20           25           30

Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
      35           40           45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
      50           55           60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
 65           70           75           80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
      85           90           95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
      100          105          110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
      115          120          125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
      130          135          140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
      145          150          155          160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
      165          170          175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
      180          185          190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
      195          200          205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
      210          215          220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
      225          230          235          240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
      245          250          255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
      260          265          270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
      275          280          285

```


Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly
 290 295 300
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala
 305 310 315 320
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala
 325 330 335
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln
 340 345 350
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met
 355 360 365
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe
 370 375 380
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala
 385 390 395 400
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp
 405 410 415
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu
 420 425 430
 Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln
 435 440 445
 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn
 450 455 460

<210> 479

<211> 984

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(961)

<223> RXN01376

<400> 479

tcctcatcgg ttatcgggag tggcggatcac ttcttgcaaa cttaaaccac tatgctttcg 60
 ctctgtgagt actttgaaat ccccatcgcc tgtgatcaca gtg acc tat tca cca 115
 Val Thr Tyr Ser Pro
 1 5
 ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
 10 15 20
 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
 25 30 35
 cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr

40	45	50	
ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser 55 60 65			307
ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu 70 75 80 85			355
gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 95 100			403
ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu 105 110 115			451
atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct ccg gcg gta ccc Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 125 130			499
act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 145			547
tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 155 160 165			595
gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp 170 175 180			643
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 195			691
atg gaa gac gtt gac ctg gga gat ccg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 205 210			739
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 215 220 225			787
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala 230 235 240 245			835
tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile 250 255 260			883
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val 265 270 275			931
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg Gly Val Ser Lys Met Arg Thr Lys Ala Ser 280 285			981

gac

984

<210> 480

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu
 1 5 10 15

Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly
 20 25 30

Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val
 35 40 45

Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn
 50 55 60

Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
 65 70 75 80

Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp
 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly
 100 105 110

Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser
 115 120 125

Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu
 130 135 140

Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp
 145 150 155 160

Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys
 165 170 175

Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu
 180 185 190

Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val
 195 200 205

Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His
 210 215 220

Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala
 225 230 235 240

His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro
 245 250 255

Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg
 260 265 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser
 275 280 285

<210> 481
 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(979)
 <223> RXN01631

<400> 481

```
gccagttgag gatgctctca cagtcgctcg cattgtcagt gcatgctacg aatccgacaa 60
caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115
                                   Met Lys Pro Gln Leu
                                   1 5
att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163
Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp
                                   10 15 20
gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211
Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala
                                   25 30 35
gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259
Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys
                                   40 45 50
gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307
Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala
                                   55 60 65
gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355
Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala
                                   70 75 80 85
act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403
Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe
                                   90 95 100
gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451
Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly
                                   105 110 115
gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499
Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe
                                   120 125 130
act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547
Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu
                                   135 140 145
gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595
Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu
                                   150 155 160 165
```

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile
 170 175 180
 tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn
 185 190 195
 att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile
 200 205 210
 gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr
 215 220 225
 tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc 835
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile
 230 235 240 245
 gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag 883
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu
 250 255 260
 cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr
 265 270 275
 acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979
 Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn
 280 285 290
 tgatctttga aaggctgaaa aaa 1002

<210> 482

<211> 293

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 482

Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala
 1 5 10 15
 Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg
 20 25 30
 Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His
 35 40 45
 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg
 50 55 60
 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu
 65 70 75 80
 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val
 85 90 95
 Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile
 100 105 110

Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His
 115 120 125
 Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly
 130 135 140
 Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile
 145 150 155 160
 Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly
 165 170 175
 Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp
 180 185 190
 Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val
 195 200 205
 Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr
 210 215 220
 Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe
 225 230 235 240
 Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu
 245 250 255
 Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln
 260 265 270
 Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu
 275 280 285
 Ala Pro Ser Thr Asn
 290

 <210> 483
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN01593

 <400> 483
 atatgacagc cttcttcttg atctagatgg aaccgtctac gagggcggcc gagccattga 60

 gcacgtagtt tctgcgtct ctggcgccgg cctaccgctc atg tat gtc acc aat 115
 Met Tyr Val Thr Asn
 1 5

 aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
 Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile
 10 15 20

 ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211
 Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala

25	30	35	
gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat			259
Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr			
40	45	50	
gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt			307
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe			
55	60	65	
gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc			355
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly			
70	75	80	85
cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca			403
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser			
90	95	100	
att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt			451
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu			
105	110	115	
ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc			499
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala			
120	125	130	
gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc			547
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly			
135	140	145	
ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct			595
Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro			
150	155	160	165
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct			643
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala			
170	175	180	
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac			691
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr			
185	190	195	
gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac			739
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His			
200	205	210	
ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc			787
Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys			
215	220	225	
cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc			835
Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe			
230	235	240	245
cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt			883
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val			
250	255	260	
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat			931
Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp			
265	270	275	

tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga 977
 Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp
 280 285

attcaccaaa gcc 990

<210> 484

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Tyr Val Thr Asn Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala
 1 5 10 15

Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met
 20 25 30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
 35 40 45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
 50 55 60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
 65 70 75 80

Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser
 85 90 95

Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn
 100 105 110

Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly
 115 120 125

Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser
 130 135 140

Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu
 145 150 155 160

Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile
 165 170 175

Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly
 180 185 190

Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro
 195 200 205

His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg
 210 215 220

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg
 225 230 235 240

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser
 245 250 255

Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr
 260 265 270

Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp
 275 280 285

Trp

<210> 485

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN00337

<400> 485

ggacgcttat tggtagcat tcggattacg ccggtggtgt ggtgctggcg gctaatacgca 60

attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115
 Met Leu Leu Thr Tyr
 1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163
 Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr
 10 15 20

gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211
 Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val
 25 30 35

ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc 259
 Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala
 40 45 50

cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307
 Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser
 55 60 65

cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355
 Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu
 70 75 80 85

ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg 403
 Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu
 90 95 100

gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451
 Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile
 105 110 115

gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499
 Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val
 120 125 130

ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att 547

Leu	Arg	Ala	Arg	His	Thr	Val	Ala	Leu	Arg	Gly	Glu	Thr	Gly	Gln	Ile	
135						140					145					
tcg	gtg	gtt	gat	tac	gcc	gat	ggg	tcg	gtc	act	cag	gcg	cca	cat	ccg	595
Ser	Val	Val	Asp	Tyr	Ala	Asp	Gly	Ser	Val	Thr	Gln	Ala	Pro	His	Pro	
150					155					160					165	
gtg	agt	cgt	tcc	gct	ggg	ttg	tcg	gca	ttt	gtt	gtt	gct	gcg	caa	act	643
Val	Ser	Arg	Ser	Ala	Gly	Leu	Ser	Ala	Phe	Val	Val	Ala	Ala	Gln	Thr	
				170					175					180		
gaa	act	gat	ccg	agc	att	tac	cgc	gag	atc	tat	gct	cga	cat	gcg	ttt	691
Glu	Thr	Asp	Pro	Ser	Ile	Tyr	Arg	Glu	Ile	Tyr	Ala	Arg	His	Ala	Phe	
			185					190					195			
atc	gat	gaa	gct	gcg	cgc	gct	ttc	agt	gtg	gaa	tct	ttg	cgg	ttg	ctt	739
Ile	Asp	Glu	Ala	Ala	Arg	Ala	Phe	Ser	Val	Glu	Ser	Leu	Arg	Leu	Leu	
		200					205					210				
ccc	gac	gct	tcc	act	cgt	gtt	gtg	gat	tgg	ttg	cag	gcc	gtg	att	gag	787
Pro	Asp	Ala	Ser	Thr	Arg	Val	Val	Asp	Trp	Leu	Gln	Ala	Val	Ile	Glu	
		215				220					225					
gtg	act	ggg	cga	gag	gat	ctg	ccc	tcg	att	gaa	caa	gcc	cag	cgc	tgg	835
Val	Thr	Gly	Arg	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Ala	Gln	Arg	Trp	
230					235					240					245	
ttg	aat	ctg	tgg	gaa	aac	gaa	acc	cgg	cgc	gct	cag	agg	aca	gcc	aat	883
Leu	Asn	Leu	Trp	Glu	Asn	Glu	Thr	Arg	Arg	Ala	Gln	Arg	Thr	Ala	Asn	
				250					255					260		
gcc	ctg	cgt	tcg	aga	agg	ctg	agt	gag	ttt	tct	gag	ctg	ctg	atg	gaa	931
Ala	Leu	Arg	Ser	Arg	Arg	Leu	Ser	Glu	Phe	Ser	Glu	Leu	Leu	Met	Glu	
			265					270					275			
tcc	caa	gat	gat	ttg	agc	gac	acc	ttc	gat	ttc	ccc	cct	gct	gat	ttg	979
Ser	Gln	Asp	Asp	Leu	Ser	Asp	Thr	Phe	Asp	Phe	Pro	Pro	Ala	Asp	Leu	
		280					285					290				
gcg	ctt	gct	cgt	ttg	tgc	gtc	gag	cgg	ggg	gcc	aca	gct	gct	cgg	tcc	1027
Ala	Leu	Ala	Arg	Leu	Cys	Val	Glu	Arg	Gly	Ala	Thr	Ala	Ala	Arg	Ser	
		295				300					305					
acg	tca	gcg	cgc	ggg	gtg	att	gcg	ttg	gtt	gat	gcc	cat	cat	gcg	cac	1075
Thr	Ser	Ala	Arg	Gly	Val	Ile	Ala	Leu	Val	Asp	Ala	His	His	Ala	His	
310					315					320					325	
aat	ttt	gct	gcg	gat	ctc	agc	gag	gat	ggc	ttg	ttg	gtg	gtt	cct	ctc	1123
Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu	Asp	Gly	Leu	Leu	Val	Val	Pro	Leu	
				330					335					340		
ggg	cac	ggg	gac	gtc	gcg	gaa	cag	ggc	tagcagcgcct	acttaaccag						1170
Gly	His	Gly	Asp	Val	Ala	Glu	Gln	Gly								
			345					350								
cct																1173
<210>	486															
<211>	350															
<212>	PRT															

<213> Corynebacterium glutamicum

<400> 486

Met Leu Leu Thr Tyr Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys
 1 5 10 15
 His Ser Leu Ser Thr Ala Asp Ile Ala Ala Arg Ala His Ala His Met
 20 25 30
 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
 35 40 45
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His
 50 55 60
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu
 65 70 75 80
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp
 85 90 95
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro
 100 105 110
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe
 115 120 125
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly
 130 135 140
 Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr
 145 150 155 160
 Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val
 165 170 175
 Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr
 180 185 190
 Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu
 195 200 205
 Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu
 210 215 220
 Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu
 225 230 235 240
 Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala
 245 250 255
 Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser
 260 265 270
 Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe
 275 280 285
 Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala
 290 295 300
 Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

305 310 315 320

Ala His His Ala His Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu
 325 330 335

Leu Val Val Pro Leu Gly His Gly Asp Val Ala Glu Gln Gly
 340 345 350

```
<210> 487
<211> 1248
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1225)
<223> RXS00584
```

<400> 487
tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60

agaggggctg cttttttggt tcttaaattc accccatccc atg cat agc cct gaa 115
Met His Ser Pro Glu
1 5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
10 15 20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
25 30 35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
40 45 50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac. 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
55 60 65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
70 75 80 85

```
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
          90                      95                      100
```

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
105 110 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
120 125 130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
 Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
 135 140 145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac	595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn	
150 155 160 165	
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct	643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala	
170 175 180	
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct	691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser	
185 190 195	
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca	739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala	
200 205 210	
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc	787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr	
215 220 225	
tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac	835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn	
230 235 240 245	
tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca	883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala	
250 255 260	
gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc	931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu	
265 270 275	
atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag	979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln	
280 285 290	
gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa	1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu	
295 300 305	
gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag	1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln	
310 315 320 325	
aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg	1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val	
330 335 340	
tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc	1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile	
345 350 355	
gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca	1219
Asp Leu Leu Ala Glu Leu Ala Ala Val Arg Glu Arg Arg Ala Ala	
360 365 370	
gcc aag taattaaggg cgctagactg tta	1248
Ala Lys	
375	

<210> 488
 <211> 375
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 488

```

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
 1           5           10           15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
      20           25           30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
      35           40           45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
      50           55           60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val
      65           70           75           80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu
      85           90           95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe
      100          105          110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro
      115          120          125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg
      130          135          140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu
      145          150          155          160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp
      165          170          175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu
      180          185          190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly
      195          200          205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His
      210          215          220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr
      225          230          235          240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
      245          250          255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly
      260          265          270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys
      275          280          285

```

Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile
 290 295 300
 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu
 305 310 315 320
 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly
 325 330 335
 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp
 340 345 350
 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg
 355 360 365
 Glu Arg Arg Ala Ala Ala Lys
 370 375

<210> 489
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXS02574

<400> 489
 tgtgctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttatt 60
 gacgtccccc tccaccctc ccgcaccgac cgcggaggat ttg gcg cgc gcg caa 115
 Leu Ala Arg Ala Gln
 1 5
 atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20
 gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35
 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50
 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65
 gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85
 ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100
 gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu	Gln	Val	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gly	Thr	Gly	Leu	Ala	Ala		
			105					110					115				
cat	ggt	gtg	aca	gtt	aac	ttt	gca	cct	gtt	gta	gat	gta	gat	gct	tgg	499	
His	Gly	Val	Thr	Val	Asn	Phe	Ala	Pro	Val	Val	Asp	Val	Asp	Ala	Trp		
		120					125				130						
ggt	ctc	ccc	gtc	gtt	ggc	gat	cgt	tcc	ttt	tcc	aac	gac	cca	gcc	gta	547	
Gly	Leu	Pro	Val	Val	Gly	Asp	Arg	Ser	Phe	Ser	Asn	Asp	Pro	Ala	Val		
	135					140					145						
gca	gct	act	tat	gcc	aca	gct	ttt	gca	aag	ggc	tta	agc	aaa	gta	gga	595	
Ala	Ala	Thr	Tyr	Ala	Thr	Ala	Phe	Ala	Lys	Gly	Leu	Ser	Lys	Val	Gly		
150					155					160					165		
att	acc	cca	gta	ttc	aaa	cat	ttc	cca	ggt	cac	ggt	cgt	gca	agt	ggc	643	
Ile	Thr	Pro	Val	Phe	Lys	His	Phe	Pro	Gly	His	Gly	Arg	Ala	Ser	Gly		
				170					175					180			
gat	tcg	cac	acc	caa	gat	gtg	gtg	acc	ccc	gca	ctt	gat	gag	ctt	aaa	691	
Asp	Ser	His	Thr	Gln	Asp	Val	Val	Thr	Pro	Ala	Leu	Asp	Glu	Leu	Lys		
			185					190					195				
act	tac	gac	ctc	atc	cct	tat	ggt	caa	gca	ctt	tct	gaa	act	gac	gga	739	
Thr	Tyr	Asp	Leu	Ile	Pro	Tyr	Gly	Gln	Ala	Leu	Ser	Glu	Thr	Asp	Gly		
		200					205					210					
gcc	gtc	atg	gtg	ggc	cac	atg	att	gtt	cca	ggt	ctt	ggc	acc	gac	gga	787	
Ala	Val	Met	Val	Gly	His	Met	Ile	Val	Pro	Gly	Leu	Gly	Thr	Asp	Gly		
	215					220					225						
gtt	cca	tcc	tct	atc	gac	ccc	gcc	acc	tat	caa	ctg	ctc	cgc	agt	ggc	835	
Val	Pro	Ser	Ser	Ile	Asp	Pro	Ala	Thr	Tyr	Gln	Leu	Leu	Arg	Ser	Gly		
230					235					240					245		
gat	tac	cca	ggt	ggc	gtg	cct	ttc	gat	ggc	gtg	atc	tac	acc	gac	gat	883	
Asp	Tyr	Pro	Gly	Gly	Val	Pro	Phe	Asp	Gly	Val	Ile	Tyr	Thr	Asp	Asp		
			250					255						260			
ctc	tct	gga	atg	agt	gcc	att	tcc	gcc	acc	cat	tca	ccc	gca	gaa	gca	931	
Leu	Ser	Gly	Met	Ser	Ala	Ile	Ser	Ala	Thr	His	Ser	Pro	Ala	Glu	Ala		
		265					270					275					
gtg	ctt	gcc	tcc	ctc	aaa	gca	ggc	gca	gac	caa	gca	cta	tgg	atc	gac	979	
Val	Leu	Ala	Ser	Leu	Lys	Ala	Gly	Ala	Asp	Gln	Ala	Leu	Trp	Ile	Asp		
		280					285					290					
tat	ggg	tcg	ttg	ggc	tcc	gcg	att	gat	cgc	gtt	gat	gct	gcc	gtt	agc	1027	
Tyr	Gly	Ser	Leu	Gly	Ser	Ala	Ile	Asp	Arg	Val	Asp	Ala	Ala	Val	Ser		
	295					300					305						
agc	ggt	gaa	tac	cct	caa	gaa	caa	atg	ctg	gca	tct	gcg	tta	aga	gtc	1075	
Ser	Gly	Glu	Tyr	Pro	Gln	Glu	Gln	Met	Leu	Ala	Ser	Ala	Leu	Arg	Val		
310					315				320						325		
caa	ttg	ctc	tac	atc	aca	cgt	ctc	gaa	caa	aag	tgaagttacc	agtc	ccgtaac	1128			
Gln	Leu	Leu	Tyr	Ile	Thr	Arg	Leu	Glu	Gln	Lys							
				330					335								
ccc																	1131

<210> 490
 <211> 336
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 490

```

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
 1              5              10              15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
      20              25              30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
      35              40              45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50              55              60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65              70              75              80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
      85              90              95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
      100             105             110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
      115             120             125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
      130             135             140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
      145             150             155             160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
      165             170             175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
      180             185             190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
      195             200             205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
      210             215             220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
      225             230             235             240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
      245             250             255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
      260             265             270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
      275             280             285

```

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 491
 <211> 1038
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> RXS03215

<400> 491

atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc	48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile	
1 5 10 15	
gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335
 tagaaactat tcagaaagca tcaccatgaa 1038

<210> 492

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 492

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
 1 5 10 15
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 493
 <211> 1031
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> FRXA01915

<400> 493

atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc	48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile	
1 5 10 15	
gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggc cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

tagaaactat tcagaaagca tca 1031

<210> 494

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
 1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 495
 <211> 1288
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXS03224

<400> 495

acgattgtgc tgctggttgc gttggtgaat agttctggac cgggtatttt gcggcgacaca 60

tggaactcat tgaacgccgc gcccggtctaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
 230 235 240 245
 ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
 250 255 260
 tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
 265 270 275
 cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290
 gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305
 ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325
 gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340
 ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355
 ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370
 atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385
 ttcaagggtgta ggggaacaaa 1288

<210> 496

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
 1 5 10 15
 Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
 20 25 30
 Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
 35 40 45
 Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65 70 75 80
 Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
 85 90 95
 Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
 100 105 110
 Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115 120 125
 Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130 135 140
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145 150 155 160
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
 165 170 175
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
 180 185 190
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195 200 205
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210 215 220
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225 230 235 240
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
 245 250 255
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
 260 265 270
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
 275 280 285
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290 295 300
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380

Ser Ala
385

<210> 497
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA00038

<400> 497
acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggttaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctg ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctg atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctg gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctg ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctg gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctg gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctg 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctg gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca	643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro	
170 175 180	
cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac	691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr	
185 190 195	
gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa	739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys	
200 205 210	
gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg	787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp	
215 220 225	
act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca	835
Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr	
230 235 240 245	
ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa	883
Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln	
250 255 260	
tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc	931
Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr	
265 270 275	
cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag	979
Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu	
280 285 290	
gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag	1027
Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu	
295 300 305	
ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc	1075
Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile	
310 315 320 325	
gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc	1123
Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val	
330 335 340	
ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga	1171
Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly	
345 350 355	
ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg	1219
Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg	
360 365 370	
atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg	1268
Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala	
375 380 385	
ttcaagggtgta ggg	1281

<210> 498

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

```

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
 1             5             10             15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
      20             25             30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
      35             40             45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
      50             55             60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65             70             75             80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
      85             90             95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
      100            105            110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115            120            125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130            135            140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145            150            155            160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
      165            170            175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
      180            185            190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195            200            205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210            215            220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225            230            235            240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
      245            250            255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
      260            265            270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
      275            280            285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290            295            300

```

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380

Ser Ala
 385

<210> 499
 <211> 517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(517)
 <223> RXC00233

<400> 499
 cgccctccagc agttgagggga gaagttccaa cacttgccacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115
 Met Ser Val Asn Glu
 1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
 105 110 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
 120 125 130

ggc cca cac cat ttc ctt 517
 Gly Pro His His Phe Leu
 135

<210> 500
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 500
 Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
 1 5 10 15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
 20 25 30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
 35 40 45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
 50 55 60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65 70 75 80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
 85 90 95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
 100 105 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
 115 120 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
 130 135

<210> 501
 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXC00236

<400> 501
 aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60
 agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt 115
 Met Val Ile Ser Phe

	1	5	
gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa	163		
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln			
10 15 20			
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt	211		
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val			
25 30 35			
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt	259		
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg			
40 45 50			
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg	307		
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala			
55 60 65			
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct	355		
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro			
70 75 80 85			
ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa	403		
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu			
90 95 100			
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg	451		
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu			
105 110 115			
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat	499		
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp			
120 125 130			
ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta	547		
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu			
135 140 145			
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att	595		
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile			
150 155 160 165			
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta	643		
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val			
170 175 180			
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg	691		
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu			
185 190 195			
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca	739		
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala			
200 205 210			
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga	787		
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg			
215 220 225			
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa	836		
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile			
230 235 240			

caagcgcaac ccc

849

<210> 502

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
 1 5 10 15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
 20 25 30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
 225 230 235 240

Ala Ile

<210> 503

<211> 1113

<212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXC00271

<400> 503

```

tagtttaaatt catgagacat ttacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgccccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
                               Met Phe Ser Ser Arg
                               1           5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
          10                15                20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
          25                30                35

ggg ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
          40                45                50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
          55                60                65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
          70                75                80                85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
          90                95                100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
          105                110                115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
          120                125                130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
          135                140                145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
          150                155                160                165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
          170                175                180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu

```

185					190					195						
ggg	ctg	tcc	gtt	aat	act	cag	act	gtc	act	acc	gtg	aac	gag	att	cag	739
Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr	Val	Asn	Glu	Ile	Gln	
200					205					210						
cag	gct	gtt	gaa	gct	ctc	ggc	gat	gtt	gat	gtc	atc	tac	gtt	cca	act	787
Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val	Ile	Tyr	Val	Pro	Thr	
215					220					225						
gac	aac	atg	gtt	gtt	tcc	ggg	att	tct	tct	ctg	gtt	cag	gtt	gct	gag	835
Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu	Val	Gln	Val	Ala	Glu	
230					235					240					245	
cag	aag	cag	atc	cct	gtg	atc	ggc	gct	gag	tcc	ggc	act	gtt	gag	ggg	883
Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser	Gly	Thr	Val	Glu	Gly	
250					255					260						
ggc	gca	ctg	gca	acc	ctg	ggg	atc	gat	tac	acc	gag	ctt	ggc	cgc	cag	931
Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr	Glu	Leu	Gly	Arg	Gln	
265					270					275						
act	ggg	gag	atg	gct	ctg	cgt	att	ctg	cag	gac	ggc	gaa	gac	cca	gca	979
Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp	Gly	Glu	Asp	Pro	Ala	
280					285					290						
acc	atg	cct	gtg	gag	act	gca	act	gag	ttc	acc	tac	gtg	atc	aac	gaa	1027
Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr	Tyr	Val	Ile	Asn	Glu	
295					300					305						
gat	gca	gca	gag	cgc	cag	ggc	gtg	gag	atc	cct	caa	gag	att	ttg	gat	1075
Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro	Gln	Glu	Ile	Leu	Asp	
310					315					320					325	
aag	gcc	gaa	cgc	gta	tgatc	ggcgc	ttttg	agattc	gga							1113
Lys	Ala	Glu	Arg	Val												
330																

<210> 504

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

Met	Phe	Ser	Ser	Arg	Ser	Lys	Val	Leu	Ala	Ser	Ile	Phe	Thr	Val	Gly	
1				5					10					15		
Ala	Leu	Ala	Leu	Ala	Ser	Cys	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Ser	Thr	
20					25					30						
Ser	Thr	Asp	Ala	Ala	Gly	Gly	Asp	Ser	Tyr	Arg	Val	Gly	Ile	Asn	Gln	
35					40					45						
Leu	Val	Gln	His	Pro	Ala	Leu	Asp	Ala	Ala	Thr	Thr	Gly	Phe	Lys	Glu	
50					55					60						
Ala	Phe	Glu	Glu	Ala	Gly	Val	Asp	Val	Thr	Phe	Asp	Glu	Gln	Asn	Ala	
65					70					75					80	
Asn	Gly	Glu	Gln	Gly	Thr	Ala	Leu	Thr	Ile	Ser	Gln	Gln	Phe	Ala	Ser	

85 .					90					95						
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala	
100					105					110						
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr	
115					120					125						
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly	
130					135					140						
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu	
145					150					155					160	
Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr	
165					170					175						
Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys	
180					185					190						
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr	
195					200					205						
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val	
210					215					220						
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu	
225					230					235					240	
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser	
245					250					255						
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr	
260					265					270						
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp	
275					280					285						
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr	
290					295					300						
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro	
305					310					315					320	
Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val							
325					330											

<210> 505

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXC00338

<400> 505

tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact 60

tg	g	g	g	a	a	a	c	g	a																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
----	---	---	---	---	---	---	---	---	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
 230 235 240 245
 gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883
 Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
 250 255 260
 ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931
 Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
 265 270 275
 cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979
 Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
 280 285 290
 tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027
 Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
 295 300 305
 gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075
 Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
 310 315 320 325
 ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123
 Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
 330 335 340
 gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171
 Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
 345 350 355
 cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
 360 365 370
 atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263
 Met Ser Ala Arg Ala Val Asn
 375 380
 <210> 506
 <211> 380
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 506
 Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
 1 5 10 15
 Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
 20 25 30
 Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45
 Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60
 Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
 85 90 95
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
 100 105 110
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
 115 120 125
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
 130 135 140
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
 145 150 155 160
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
 165 170 175
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
 180 185 190
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
 195 200 205
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
 210 215 220
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
 225 230 235 240
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
 245 250 255
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
 260 265 270
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
 275 280 285
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
 290 295 300
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
 305 310 315 320
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
 325 330 335
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
 340 345 350
 Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
 355 360 365
 Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
 370 375 380

<210> 507

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXC00362

<400> 507

```

cactttttgg gtgaaaattc cacgaagtta atgccgcttt aagtcaattc aatcacatgt 60
aacatgctac ggtttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct 115
                                         Met Gly Ile Ile Ala
                                         1 5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                        10                        15                        20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
                        25                        30                        35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
                        40                        45                        50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
                        55                        60                        65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
                        70                        75                        80                        85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                        90                        95                        100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
                        105                        110                        115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
                        120                        125                        130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
                        135                        140                        145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
                        150                        155                        160                        165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                        170                        175                        180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt 691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
                        185                        190                        195

```


tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg	739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg	
200 205 210	
gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc	787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
215 220 225	
ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct	835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
230 235 240 245	
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
280 285 290	
atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt	1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg	1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg	1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu	
375 380 385	
tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac	1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr	
390 395 400 405	
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca	1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro	
410 415 420	
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt	1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val	
425 430 435	

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
 440 445

aaaatgaact caa 1470

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
 1 5 10 15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
 20 25 30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
 180 185 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
 195 200 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
 210 215 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
 225 230 235 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
 245 250 255

Gly	Val	Lys	Ser	Met	Ser	Ile	Ile	Val	Trp	Val	Pro	Ile	Leu	Ile	Thr	260	265	270
Ala	Ile	Ala	Leu	Ile	Glu	Gly	Arg	Lys	Arg	Ile	Ala	Asn	Asn	Met	Ala	275	280	285
His	Phe	Arg	Val	Gln	Ile	Ser	Lys	Asp	Leu	Pro	Gln	Phe	Ala	Thr	Val	290	295	300
Gly	Ile	Ser	Leu	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Asn	Ile	Met	Glu	Glu	305	310	315
Leu	Gly	Val	Gly	Pro	Gln	Leu	Ser	Asn	Trp	Leu	Asp	Ser	Met	Asp	Leu	325	330	335
Pro	Lys	Ser	Val	Met	Val	Ile	Ile	Val	Cys	Ile	Met	Cys	Ile	Val	Val	340	345	350
Ala	Thr	Pro	Leu	Ser	Ser	Thr	Ala	Thr	Ala	Ala	Ala	Ile	Gly	Ala	Pro	355	360	365
Ala	Val	Ala	Ala	Leu	Ala	Ala	Val	Gly	Ile	Asp	Pro	Thr	Val	Ala	Ile	370	375	380
Val	Val	Ile	Leu	Leu	Cys	Thr	Ser	Thr	Glu	Gly	Ala	Ser	Pro	Pro	Val	385	390	395
Gly	Ala	Pro	Ile	Tyr	Leu	Ser	Ala	Ala	Ile	Ala	Asp	Ala	Asn	Pro	Thr	405	410	415
Lys	Met	Phe	Val	Pro	Leu	Ile	Thr	Tyr	Phe	Val	Val	Pro	Met	Ile	Leu	420	425	430
Leu	Ala	Trp	Leu	Val	Gly	Met	Gly	Phe	Leu	Pro	Val	Ile	Val	Pro	Thr	435	440	445

Gly

```
<210> 509
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1180)  
<223> RXC00412
```

```

<400> 509
cttttgacga acaccacgtc gcgtacgctt cctcggggcg ttaaactatt tgtcttccag 60

cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
                                         Val Ser His Thr Ala
                                         1                               5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
          10                      15                      20

```

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat	211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn	
25 30 35	
aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa	259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu	
40 45 50	
ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc	307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser	
55 60 65	
act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg	355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser	
70 75 80 85	
ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg	403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu	
90 95 100	
cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg	451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu	
105 110 115	
ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt	499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val	
120 125 130	
gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc	547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu	
135 140 145	
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg	595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu	
150 155 160 165	
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc	643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr	
170 175 180	
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca	691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro	
185 190 195	
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa	739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu	
200 205 210	
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt	787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg	
215 220 225	
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa	835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu	
230 235 240 245	
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct	883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala	
250 255 260	
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa	931

Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203
 Ile Thr Arg
 360

<210> 510
 <211> 360
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510
 Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
 115 120 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
 130 135 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
 145 150 155 160
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
 165 170 175
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
 180 185 190
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
 195 200 205
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
 210 215 220
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
 225 230 235 240
 Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
 245 250 255
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
 260 265 270
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
 275 280 285
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
 290 295 300
 Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
 305 310 315 320
 Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
 325 330 335
 Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
 340 345 350
 Thr Thr Ile Lys Glu Ile Thr Arg
 355 360

<210> 511
 <211> 813
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXC00526

<400> 511
 ggtggagcag gggcgggctc ctttagtcc tgcggcccct tttgaccctg cagcccctgc 60
 cgtttctgcc aagcaaaccg tgggccaggt gatttagcct atg agc ctc atc gaa 115
 Met Ser Leu Ile Glu
 1 5
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163

Met	Arg	Asn	Ile	Val	Lys	Thr	Tyr	Asn	Ile	Gly	Ser	Glu	Gly	Glu	Leu	
				10					15					20		
acc	gtg	ttg	cac	ggt	gtg	gat	ttc	cat	gtg	gac	cgt	ggc	gaa	ttc	gtg	211
Thr	Val	Leu	His	Gly	Val	Asp	Phe	His	Val	Asp	Arg	Gly	Glu	Phe	Val	
			25					30					35			
tcg	gtt	gtg	ggt	acg	tcc	ggc	tca	ggt	aaa	tca	acg	atg	atg	aac	atc	259
Ser	Val	Val	Gly	Thr	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Met	Met	Asn	Ile	
		40					45					50				
att	ggg	ttg	ttg	gat	aag	cca	act	gat	ggc	acg	tac	acc	ttg	gat	ggc	307
Ile	Gly	Leu	Leu	Asp	Lys	Pro	Thr	Asp	Gly	Thr	Tyr	Thr	Leu	Asp	Gly	
	55					60					65					
gtg	gat	gtg	ttg	gat	atc	agc	gat	gat	gct	ttg	gcg	agc	cac	cgc	gct	355
Val	Asp	Val	Leu	Asp	Ile	Ser	Asp	Asp	Ala	Leu	Ala	Ser	His	Arg	Ala	
	70				75					80					85	
aaa	tcg	att	ggt	ttt	gtg	ttt	cag	aac	ttc	aat	ctg	att	ggc	cgg	atc	403
Lys	Ser	Ile	Gly	Phe	Val	Phe	Gln	Asn	Phe	Asn	Leu	Ile	Gly	Arg	Ile	
			90						95					100		
gat	gcg	ttg	aag	aat	gtg	gaa	atg	ccc	atg	atg	tat	gcg	ggc	att	ccg	451
Asp	Ala	Leu	Lys	Asn	Val	Glu	Met	Pro	Met	Met	Tyr	Ala	Gly	Ile	Pro	
			105					110					115			
gct	aag	cag	cgg	aga	agt	cgt	gcg	gtt	gaa	tta	ttg	gaa	atg	gtc	ggg	499
Ala	Lys	Gln	Arg	Arg	Ser	Arg	Ala	Val	Glu	Leu	Leu	Glu	Met	Val	Gly	
		120					125					130				
atg	ggt	gag	cgt	ctc	aac	cat	gag	ccc	aat	gag	ctt	tcg	ggt	ggt	cag	547
Met	Gly	Glu	Arg	Leu	Asn	His	Glu	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	
	135					140					145					
aag	cag	cgc	gtg	gcc	att	gct	cgc	gcg	ttg	gcg	aac	gat	cct	gag	atc	595
Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Asn	Asp	Pro	Glu	Ile	
	150				155				160						165	
att	ctt	gct	gat	gaa	cca	act	ggt	gcg	ttg	gat	tct	gca	acg	ggc	cgg	643
Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Ala	Thr	Gly	Arg	
			170					175						180		
atg	gtg	atg	gat	att	ttc	cac	cag	ctc	aac	aag	gag	cag	ggc	aaa	acc	691
Met	Val	Met	Asp	Ile	Phe	His	Gln	Leu	Asn	Lys	Glu	Gln	Gly	Lys	Thr	
			185					190					195			
atc	gtg	ttt	att	act	cac	aac	cct	gag	ctt	gct	gat	gaa	tct	gat	cgg	739
Ile	Val	Phe	Ile	Thr	His	Asn	Pro	Glu	Leu	Ala	Asp	Glu	Ser	Asp	Arg	
		200					205					210				
gtg	gtc	acc	atg	gtt	gac	ggg	cgc	atc	att	ggg	tct	gag	gtg	aaa	cac	787
Val	Val	Thr	Met	Val	Asp	Gly	Arg	Ile	Ile	Gly	Ser	Glu	Val	Lys	His	
		215				220					225					
tca	tgagccttgc	agaatcaatt	ctt													813
Ser																
230																

<210> 512

<211> 230
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 512

```

Met Ser Leu Ile Glu Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly
 1           5           10           15

Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
      20           25           30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
      35           40           45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
 50           55           60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65           70           75           80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
      85           90           95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
      100          105          110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
 115          120          125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
 130          135          140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
 145          150          155          160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
      165          170          175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
      180          185          190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
      195          200          205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
 210          215          220

Ser Glu Val Lys His Ser
 225          230

```

<210> 513
 <211> 1185
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1162)
 <223> RXC01004

<400> 513

ccggacgctg gatcgacgca gtaacgggtca tggaagatcg acgcatcgac aaagccgttc 60

tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
 Val Ser Ile Trp Ala
 1 5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
 Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
 10 15 20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
 Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
 25 30 35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
 Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
 40 45 50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
 Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
 55 60 65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
 Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
 70 75 80 85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
 Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
 90 95 100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
 Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
 105 110 115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
 Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
 120 125 130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
 Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
 135 140 145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
 Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
 150 155 160 165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
 Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
 170 175 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
 Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
 185 190 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
 Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
 200 205 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
 Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr

215	220	225	
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca			835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala			
230	235	240	245
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga			883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly			
	250	255	260
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct			931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala			
	265	270	275
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc			979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg			
	280	285	290
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat			1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp			
	295	300	305
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt			1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly			
310	315	320	325
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg			1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val			
	330	335	340
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt			1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp			
	345	350	
aactgtgttg gac			1185
.			
<210> 514			
<211> 354			
<212> PRT			
<213> Corynebacterium glutamicum			
.			
<400> 514			
Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala			
1	5	10	15
Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg			
	20	25	30
Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys			
	35	40	45
Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln			
	50	55	60
Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro			
	65	70	75
			80
Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro			
	85	90	95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
 100 105 110
 Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
 115 120 125
 Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
 130 135 140
 Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
 145 150 155 160
 Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
 165 170 175
 Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
 180 185 190
 Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
 195 200 205
 Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
 210 215 220
 Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
 225 230 235 240
 Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
 245 250 255
 Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
 260 265 270
 Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
 275 280 285
 Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
 290 295 300
 Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
 305 310 315 320
 Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
 325 330 335
 Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
 340 345 350

Asp Asp

<210> 515

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXC01017

<400> 515

gaaatttgag	ggggcgctac	ccttagaagg	tgcgcgaatga	caccacgata	gttcgcgcct	60
agtgtggatt	gctagaaaac	tttaagaaag	aggaaataat	atg gct caa aaa gta	115	
				Met Ala Gln Lys Val		
				1 5		
acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc	163					
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg						
10 15 20						
tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt	211					
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val						
25 30 35						
cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat	259					
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp						
40 45 50						
tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca	307					
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala						
55 60 65						
gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca	355					
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala						
70 75 80 85						
atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc	403					
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser						
90 95 100						
ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct	451					
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala						
105 110 115						
gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc	499					
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg						
120 125 130						
gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc	547					
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr						
135 140 145						
cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc	595					
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr						
150 155 160 165						
cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc	643					
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe						
170 175 180						
aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act	691					
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr						
185 190 195						
gag aac cca cag ttc gac taattaacgc tgtctctgct tat	732					
Glu Asn Pro Gln Phe Asp						
200						

<210> 516
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 516

```

Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
  1              5              10              15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
              20              25              30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
              35              40              45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
              50              55              60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
              65              70              75              80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
              85              90              95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
              100             105             110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
              115             120             125

Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
              130             135             140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
              145             150             155             160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
              165             170             175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
              180             185             190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
              195             200
  
```

<210> 517
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622)
 <223> RXC01021

<400> 517

```

cgagaggctt ttttggtctt aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
              Met Ser Ser Ser Glu
  
```

															1																5
agc	tcg	cgt	tcc	gaa	ggc	tcg	cag	cca	gca	ccg	tct	gta	cag	cct	gaa	163															
Ser	Ser	Arg	Ser	Glu	Gly	Ser	Gln	Pro	Ala	Pro	Ser	Val	Gln	Pro	Glu																
				10					15					20																	
cgc	cgt	gct	gat	tca	acg	ggg	gct	cct	gcg	gca	gct	tcc	aag	gaa	gct	211															
Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala	Ala	Ser	Lys	Glu	Ala																
				25					30					35																	
tcc	caa	caa	atg	gac	gct	gcc	gga	gtt	ctt	gag	tg	gcc	agg	acc	gct	259															
Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu	Trp	Ala	Arg	Thr	Ala																
				40					45					50																	
gtc	gag	cag	ctt	tct	gaa	cgt	cgt	gca	gag	atc	aat	gca	ctg	aat	gtc	307															
Val	Glu	Gln	Leu	Ser	Glu	Arg	Arg	Ala	Glu	Ile	Asn	Ala	Leu	Asn	Val																
				55					60					65																	
ttt	cct	gtt	cca	gat	gca	gac	act	gga	tca	aac	atg	acc	tac	acc	atg	355															
Phe	Pro	Val	Pro	Asp	Ala	Asp	Thr	Gly	Ser	Asn	Met	Thr	Tyr	Thr	Met																
				70					75					80																	
aca	gct	gcg	ttg	gat	gaa	gcg	ctg	aaa	ctg	ggg	gag	ttg	ggt	gat	gtc	403															
Thr	Ala	Ala	Leu	Asp	Glu	Ala	Leu	Lys	Leu	Gly	Glu	Leu	Gly	Asp	Val																
				90					95					100																	
gca	agg	att	act	gag	gct	ttg	gct	gtt	ggt	tct	gtg	cgt	gga	gcc	cga	451															
Ala	Arg	Ile	Thr	Glu	Ala	Leu	Ala	Val	Gly	Ser	Val	Arg	Gly	Ala	Arg																
				105					110					115																	
gga	aat	tct	gga	gta	gtc	ctt	agt	cag	gtc	ctt	cgc	gct	att	gct	cag	499															
Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu	Arg	Ala	Ile	Ala	Gln																
				120					125					130																	
gca	gct	gct	gac	ggg	gtt	att	gat	ggc	cac	aca	atc	caa	gaa	gcg	cta	547															
Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr	Ile	Gln	Glu	Ala	Leu																
				135					140					145																	
tcc	att	gct	cgc	tcc	cta	gtt	gat	cgc	gca	att	aca	gat	cct	gtg	gag	595															
Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile	Thr	Asp	Pro	Val	Glu																
				150					155					160																	
ggc	act	gtt	gtc	act	gtg	ttg	cgt	tct								622															
Gly	Thr	Val	Val	Thr	Val	Leu	Arg	Ser																							
				170																											

<210> 518

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Met	Ser	Ser	Ser	Glu	Ser	Ser	Arg	Ser	Glu	Gly	Ser	Gln	Pro	Ala	Pro
1				5					10					15	

Ser	Val	Gln	Pro	Glu	Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala
			20					25					30		

Ala	Ser	Lys	Glu	Ala	Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu
		35					40					45			

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
 50 55 60
 Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65 70 75 80
 Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
 85 90 95
 Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
 100 105 110
 Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
 115 120 125
 Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
 130 135 140
 Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
 145 150 155 160
 Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
 165 170

<210> 519
 <211> 1047
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1024)
 <223> RXC01212

<400> 519
 tttagaagcc acatgacata tgtcatgaaa attatgtgca aagtcagta atactcctga 60
 catatggctc taccagcgcc aatgcgaagt aggaagaatt atg cct atg aca acg 115
 Met Pro Met Thr Thr
 1 5
 aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
 Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
 10 15 20
 acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
 Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
 25 30 35
 ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
 40 45 50
 atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307
 Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
 55 60 65
 ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355
 Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile

70	75	80	85	
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc	403			
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr				
90 95 100				
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat	451			
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp				
105 110 115				
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc	499			
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly				
120 125 130				
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg	547			
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu				
135 140 145				
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc	595			
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu				
150 155 160 165				
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa	643			
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys				
170 175 180				
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc	691			
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala				
185 190 195				
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca	739			
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala				
200 205 210				
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc	787			
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile				
215 220 225				
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg	835			
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly				
230 235 240 245				
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc	883			
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr				
250 255 260				
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg	931			
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly				
265 270 275				
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta	979			
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val				
280 285 290				
ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc	1024			
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala				
295 300 305				
tagaatcttt aaggagacca caa	1047			

<210> 520

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 520

```

Met Pro Met Thr Thr Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg
 1             5             10             15

Thr Tyr Gly Asp Tyr Thr Ala Val Lys Gly Leu Asn Phe His Val Gln
      20             25             30

Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
      35             40             45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
      50             55             60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
      65             70             75             80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
      85             90             95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
      100            105            110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
      115            120            125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
      130            135            140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
      145            150            155            160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
      165            170            175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
      180            185            190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
      195            200            205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
      210            215            220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
      225            230            235            240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
      245            250            255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
      260            265            270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
      275            280            285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser

```

290

295

300

Leu Gln Thr Ala
305

<210> 521

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1108)

<223> RXC01306

<400> 521

tgtttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60

cccagacaat caccocgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat 115
Met Thr Glu Trp Tyr
1 5

gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
10 15 20

gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
25 30 35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
40 45 50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
55 60 65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70 75 80 85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
90 95 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
105 110 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
120 125 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
135 140 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val

150	155	160	165	
cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat				643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr				
170		175	180	
gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc				691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly				
185		190	195	
gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg				739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu				
200		205	210	
gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac				787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His				
215		220	225	
agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt				835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser				
230		235	240	245
ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac				883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His				
250		255	260	
gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct				931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala				
265		270	275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta				979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu				
280		285	290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg				1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala				
295		300	305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat				1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp				
310		315	320	325
cac atc ttg aaa tac ctg tgg cct gca tog gtg tagctaattt gaggtgcgct				1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val				
330		335		
gaa				1131
<210> 522				
<211> 336				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 522				
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala				
1	5	10	15	
Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg				
20	25	30		

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
 180 185 190
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
 195 200 205
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
 210 215 220
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
 225 230 235 240
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
 245 250 255
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
 260 265 270
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
 275 280 285
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
 290 295 300
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
 305 310 315 320
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 325 330 335